

SEQUENCE LISTING

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<120> Mu-Conopeptides

<130> 2314-242

<150> US 60/219,619

<151> 2000-07-21

<150> US 60/245,157

<151> 2000-11-03

<150> US 60/264,319

<151> 2001-01-29

<150> US 60/277,270

<151> 2001-03-21

<160> 520

<170> PatentIn version 3.0

<210> 1

<211> 280

<212> DNA

<213> Conus arentus

<400> 1

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agagcgtatg caggacgact ttataactga gcatcatccc ctgtttgatc ctgtcaaacg      180
gtgttgcgag aggccatgca acataggatg cgtaccttgt tgtaaatgac cagctttgtc      240
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<210> 2

<211> 67

<212> PRT

<213> Conus arentus

<400> 2

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Met Met Ser Lys Leu Gly Val Phe Leu Thr Ile Cys Met Leu Leu Phe
1           5           10           15

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Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
          20          25          30

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Ala Glu Arg Met Gln Asp Asp Phe Ile Thr Glu His His Pro Leu Phe

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2000-07-21 2000-11-03 2001-01-29 2001-03-21

45

Pro Cys Cys
65

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<210> 3
<211> 14
<212> PRT
<213> Conus arentus

<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5 and
      d 12 is Pro or Hy

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<400> 3
Cys Cys Xaa Arg Xaa Cys Asn Ile Gly Cys Val Xaa Cys Cys
1 5 10

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<210> 4
<211> 244
<212> DNA
<213> Conus atlanticus
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<400>      4
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atttcatctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc      180
gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct      240
cgag                                          244

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<210> 5
<211> 69
<212> PRT
<213> Conus atlanticus
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<400> 5
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Val His
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
35 40 45

Phe Asp Leu Ile Lys Arg Cys Cys Glu Leu Pro Cys Gly Pro Gly Phe
50 55 60

Cys Val Pro Cys Cys
65

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<210> 6
<211> 15
<212> PRT
<213> Conus atlanticus
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<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
 and 13 is Pro or Hy

<400> 6
 Cys Cys Xaa Leu Xaa Cys Gly Xaa Gly Phe Cys Val Xaa Cys Cys
 1 5 10 15

<210> 7
 <211> 310
 <212> DNA
 <213> Conus aurisiacus

<400> 7
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 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttaatc agaaaagaat 180
 gtgttgccgc gaaggccgga aatgccccag ctatttcaga aacagtcaga tttgtcattg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcgttatca cgactaatga ataagtaaaa 300
 cgattgcagt 310

<210> 8
 <211> 74
 <212> PRT
 <213> Conus aurisiacus

<400> 8
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30
 Glu Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45
 Asn Gln Lys Arg Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr
 50 55 60
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 9
 <211> 22
 <212> PRT
 <213> Conus aurisiacus
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
 s Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr,
 di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 9
 Met Cys Cys Gly Xaa Gly Arg Lys Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys

<400> 13
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<210> 14
<211> 78
<212> PRT
<213> Conus aurisiacus
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Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
20 25 30

Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
50 55 60

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<210> 15
<211> 23
<212> PRT
<213> Conus aurisiacus
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<220>
<221>  PEPTIDE
<222>  (1)..(23)
<223>  Xaa at residue 1 is Gln or pyro-Glu
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Lys Asn Leu Lys Cys Cys Ser
20

<210>	16
<211>	232
<212>	DNA
<213>	Conus aurisiacus

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<400> 16
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ggcatttcac ctaaacgcca tccctggttt gatcccgta aacgggtgtg caaggtgcaa 180
tgcgagtctt gcacccttgg ttgctaacgt gttgatgacc aactttctcg ag 232

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<210> 17
<211> 68
<212> PRT
<213> Conus aurisiacus
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<400>      20
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Met Leu
1          5          10          15
Leu Phe Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp
20          25          30
Arg Pro Ala Glu Arg Ser Gln Asp Val Ser Ser Glu Gln His Pro Leu
35          40          45
Phe Asp Pro Val Lys Arg Cys Cys Asn Trp Pro Cys Ser Met Gly Cys
50          55          60

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Ile Pro Cys Cys Tyr Tyr
65 70

<210> 21
<211> 16
<212> PRT
<213> Conus bandus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 4 is Trp or
bromo-Trp; Xaa at residue 15 and 16 is Tyr, 125I-Tyr, mono-iodo-
Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 21
Cys Cys Asn Xaa Xaa Cys Ser Met Gly Cys Ile Xaa Cys Cys Xaa Xaa
1 5 10 15

<210> 22
<211> 298
<212> DNA
<213> Conus betulinus

<400> 22
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gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120
agagcgtatg caggacattt catctgaaca gcatcccttg tttgatcccg tcaaacgggtg 180
ttgcgaattg ccatgccatg gatgcgtccc ttgttgctgg ccttaataac gtgtggatga 240
ccaactgtgt tatcacggcc acgtcaagtg tctaataaat aagtaaaatg attgcagt 298

<210> 23
<211> 67
<212> PRT
<213> Conus betulinus

<400> 23
Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Ile Ser Ser Glu Gln His Pro Leu Phe Asp
35 40 45

Pro Val Lys Arg Cys Cys Glu Leu Pro Cys His Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro
65

<210> 24
<211> 15
<212> PRT
<213> Conus betulinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 1

Parameter	Value	Unit
Initial concentration of Fe^{2+}	0.001	M
Initial concentration of Fe^{3+}	0.001	M
Initial concentration of Fe^{2+} and Fe^{3+}	0.002	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+}	0.003	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+}	0.004	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+}	0.005	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+} and Fe^{7+}	0.006	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+} and Fe^{7+} and Fe^{8+}	0.007	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+} and Fe^{7+} and Fe^{8+} and Fe^{9+}	0.008	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+} and Fe^{7+} and Fe^{8+} and Fe^{9+} and Fe^{10+}	0.009	M
Initial concentration of Fe^{2+} and Fe^{3+} and Fe^{4+} and Fe^{5+} and Fe^{6+} and Fe^{7+} and Fe^{8+} and Fe^{9+} and Fe^{10+} and Fe^{11+}	0.010	M

Cys Cys Xaa Leu Xaa Cys His Gly Cys Val Xaa Cys Cys Xaa Xaa
1 5 10 15

<213> *Conus betulinus*

ccaactttgt tatcacggcc acgtcaagtg tctgatgaat aagtaaaacg attgcagt 298

<213> Conus betulinus

Met Met Ser Lys Leu Gly Val Leu Leu Thr Phe Cys Leu Leu Leu Phe
1 5 10 15

Ala Glu Arg Met Gln Asp Ile Ser Pro Glu Gln His Pro Ser Phe Asp

Pro Val Lys Arg Cys Cys Gly Leu Pro Cys Asn Gly Cys Val Pro Cys
50 55 60

Cys Trp Pro Ser
65

<213> Conus betulinus

<223> Xaa at residue 5, 11 and 15 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Trp

Cys Cys Gly Leu Xaa Cys Asn Gly Cys Val Xaa Cys Cys Xaa Xaa Ser
1 5 10 15

<213> Conus betulinus

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gcttctgttt ccctttactg ctcttccgct ggatggagat caacctgcag accaacctct 120
 agagcgcgatg cagtatgaca tggtacgtgc agtgaatccc tggtttgatc ccgtcaaaag 180
 gtgctgctcg aggaactgcy cagtatgcat cccttggtgc ccgaattggc cagcttgatt 240
 atcgcggccca agagtctaata gaataagtaa aacgattgca gt 282

<210> 29
 <211> 71
 <212> PRT
 <213> Conus betulinus

<400> 29
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Tyr Met Leu Leu Phe
 1 5 10 15
 Pro Phe Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30
 Leu Glu Arg Met Gln Tyr Asp Met Leu Arg Ala Val Asn Pro Trp Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Pro
 50 55 60
 Cys Cys Pro Asn Trp Pro Ala
 65 70

<210> 30
 <211> 18
 <212> PRT
 <213> Conus betulinus
 <220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 11, 14 and 17 is Pro or Hyp; Xaa at residue 16 is
 Trp or bromo-Trp

<400> 30
 Cys Cys Ser Arg Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa Asn Xaa
 1 5 10 15

Xaa Ala

<210> 31
 <211> 325
 <212> DNA
 <213> Conus bullatus

<400> 31
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 agagcgtatg caggacgaca tttcatctga gcagaattcc ttgcttgaga agagagttac 180
 tgacaggtgc tgcaaaggga agagggaatg cggcagatgg tgcagagatc actcgcggtg 240
 ttgcggtcga cgataagctg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300
 agtgaataag taaaatgatt gcagt 325

<210> 32

<211> 77
 <212> PRT
 <213> Conus bullatus

<400> 32
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Asn Ser Leu Leu
 35 40 45
 Glu Lys Arg Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Glu Cys Gly
 50 55 60
 Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 33
 <211> 23
 <212> PRT
 <213> Conus bullatus
 <220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 11 is Glu or gamma-carboxy Glu; Xaa at residue 15
 is Trp or bromo-Trp

<400> 33
 Val Thr Asp Arg Cys Cys Lys Gly Lys Arg Xaa Cys Gly Arg Xaa Cys
 1 5 10 15
 Arg Asp His Ser Arg Cys Cys
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<210> 34
 <211> 326
 <212> DNA
 <213> Conus bullatus

<400> 34
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 agagcgtatg caggatgaca tttcatctga gcagaatccc ttgcttgaga agagagttgg 180
 tgacaggtgc tgcaaaggga agaggggggtg cggcagatgg tgcagagatc actcacgttg 240
 ttgcggtcga cgataacgtg ttgatgacca gctttgttat cacggctaca tcaagtgtct 300
 tagtgattaa gtaaaacgat tgcagt 326

<210> 35
 <211> 77
 <212> PRT
 <213> Conus bullatus

<400> 35
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Gly Arg Trp Cys Arg Asp His Ser Arg Cys Cys Gly Arg Arg

65

70

75

<210> 39

<211> 24

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 16 is Trp or bromo-Trp

<400> 39

Val	Gly	Xaa	Arg	Cys	Cys	Lys	Asn	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Xaa
1				5					10					15	

Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
			20				

<210> 40

<211> 337

<212> DNA

<213> Conus bullatus

<400> 40

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agagcgtatg	caggacgacc	tttcatctga	gcagcatccc	ttgtttgaga	agagaattgt	180
tgacaggtgc	tgcaacaaag	ggaacgggaa	gaggggggtgc	agcagatggt	gcagagatca	240
ctcacgttgt	tgcggtcgac	gatgaactgt	tgatgaccga	ggcttttggtt	atcacggcta	300
catcaagtgt	ctagtgaata	agtaaaacga	ttgcagt			337

<210> 41

<211> 80

<212> PRT

<213> Conus bullatus

<400> 41

Met	Met	Ser	Lys	Leu	Gly	Val	Leu	Leu	Thr	Ile	Cys	Leu	Leu	Leu	Phe
1				5					10					15	

Pro	Leu	Phe	Ala	Leu	Pro	Gln	Asp	Gly	Asp	Gln	Pro	Ala	Asp	Arg	Pro
			20					25					30		

Ala	Glu	Arg	Met	Gln	Asp	Asp	Leu	Ser	Ser	Glu	Gln	His	Pro	Leu	Phe
			35				40					45			

Glu	Lys	Arg	Ile	Val	Asp	Arg	Cys	Cys	Asn	Lys	Gly	Asn	Gly	Lys	Arg
	50					55					60				

Gly	Cys	Ser	Arg	Trp	Cys	Arg	Asp	His	Ser	Arg	Cys	Cys	Gly	Arg	Arg
65					70					75				80	

<210> 42

<211> 26

<212> PRT

<213> Conus bullatus

<220>

<221> PEPTIDE
 <222> (1)..(26)
 <223> Xaa at residue 18 is Trp or bromo-Trp

<400> 42
 Ile Val Asp Arg Cys Cys Asn Lys Gly Asn Gly Lys Arg Gly Cys Ser
 1 5 10 15

Arg Xaa Cys Arg Asp His Ser Arg Cys Cys
 20 25

<210> 43
 <211> 337
 <212> DNA
 <213> Conus bullatus

<400> 43
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 gcttctgttt cccctttttg ctcttcgcga ggatggagat caacctgcag accgacctgc 120
 tgagcgtatg caggacgaca ttcatctga gcggaatccc ttgtttgaga agagcggttg 180
 tttatattgc tgccgacca aacccaacgg gcagatgatg tgcgacagat ggtgcaaaaa 240
 aaactcacgt tgttgcggtc gacgataatg tgttgatgac cagctttgtt atcaaggcta 300
 catcaagtat ctagtgaata agtaaaacga ttgcagt 337

<210> 44
 <211> 77
 <212> PRT
 <213> Conus bullatus

<400> 44
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Phe Ala Leu Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asn Pro Leu Phe Glu Lys
 35 40 45

Ser Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp
 50 55 60

Arg Trp Cys Glu Lys Asn Ser Arg Cys Cys Gly Arg Arg
 65 70 75

<210> 45
 <211> 27
 <212> PRT
 <213> Conus bullatus

<220>
 <221> PEPTIDE
 <222> (1)..(27)
 <223> Xaa at residue 21 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 19 is Trp or bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 45
 Val Gly Leu Xaa Cys Cys Arg Xaa Lys Xaa Asn Gly Gln Met Met Cys

```

1           5           10           15
Asp Arg Xaa Cys Xaa Lys Asn Ser Arg Cys Cys
      20           25

<210> 46
<211> 323
<212> DNA
<213> Conus bullatus
<400> 46
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agaacgtatg caggacgacc tttcatctga gcagcatccc ttgtttgttc agaaaagaag      180
gtgttgcggc gaaggcttga catgccccag atattggaaa aacagtcaga tttgtgcttg      240
ttgttaaatg acaacgtgtc gatgaccaac ttcggtatca cgactacgcc aagtgtctaa      300
tgaataagta aaacgattgc agt                                         323

<210> 47
<211> 74
<212> PRT
<213> Conus bullatus

<400> 47
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1           5           10           15
Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Val Asp Arg Pro
      20           25           30
Ala Glu Arg Met Gln Asp Asp Leu Ser Ser Glu Gln His Pro Leu Phe
      35           40           45
Val Gln Lys Arg Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr
      50           55           60
Trp Lys Asn Ser Gln Ile Cys Ala Cys Cys
65           70

<210> 48
<211> 22
<212> PRT
<213> Conus bullatus

<220>
<221> PEPTIDE
<222> (1)..(22)
<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 10 i
s Pro or Hyp; Xaa at residue 13 is Trp or bromo-Trp; Xaa at resid
ue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr
or O-phospho-Ty

<400> 48
Arg Cys Cys Gly Xaa Gly Leu Thr Cys Xaa Arg Xaa Xaa Lys Asn Ser
1           5           10           15
Gln Ile Cys Ala Cys Cys
      20

<210> 49
<211> 322

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gacagttcag ctgccctgat caatacctgg attgatcatt cccattcttg ctgcaggac 180

tgcggtgaag attgtgttg ttgttgccgg taacgtgttg atgaccaact ttctcgag 238

<210> 53

<211> 70

<212> PRT

<213> Conus capitaneus

<400> 53

Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asn Gln Pro Ala Asp
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
35 40 45

Thr Trp Ile Asp His Ser His Ser Cys Cys Arg Asp Cys Gly Glu Asp
50 55 60

Cys Val Gly Cys Cys Arg
65 70

<210> 54

<211> 15

<212> PRT

<213> Conus capitaneus

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> Xaa at residue 8 is Glu or gamma-carboxy Glu

<400> 54

Ser Cys Cys Arg Asp Cys Gly Xaa Asp Cys Val Gly Cys Cys Arg
1 5 10 15

<210> 55

<211> 323

<212> DNA

<213> Conus characteristicus

<400> 55

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gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca ttcatctga gcagtatccc ttgtttgata tgagaaaaag 180

gtgttgccgg cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaagt acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataagta aaatgattgc agt 323

<210> 56

<211> 74

<212> PRT

<213> Conus characteristicus

<400> 56

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 57

<211> 21

<212> PRT

<213> Conus characteristicus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue 11 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 57

Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
20

<210> 58

<211> 316

<212> DNA

<213> Conus characteristicus

<400> 58

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60

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cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180

ttgttgact cgcgcaaga aatgcaaaga ccgacaatgc aaaccccaga gatgttgcg 240

tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgt tagtgaataa 300

gtaaaatgat tgcagt 316

<210> 59

<211> 75

<212> PRT

<213> Conus characteristicus

<400> 59

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe

115 120 180 240 300 316

$\langle 210 \rangle$	63
$\langle 211 \rangle$	18

<400> 63
Arg Cys Cys Arg Xaa Xaa Cys Xaa Asp Ser Cys His Gly Ser Cys Cys
1 5 10 15

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<210> 64
<211> 292
<212> DNA
<213> Conus characteristicus
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<210> 65
<211> 69
<212> PRT
<213> Conus characteristicus
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Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
50 55 60

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<210> 66
<211> 15
<212> PRT
<213> Conus characteristicus
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<400> 66
Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Lys Xaa Cys Cys

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1              5              10              15
<210> 67
<211> 293
<212> DNA
<213> Conus characteristicus

<400> 67
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acttctgttt tccctaactg ctgttcgcgt ggatggagat caacatgcag accaacctgc      120
agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgata ccggtcaaacg      180
gtgttgcatg gattcggaat gcgactattc ttgctggcct tgctgtatgt ttggataacc      240
tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt          293

<210> 68
<211> 71
<212> PRT
<213> Conus characteristicus

<400> 68
Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1              5              10              15
Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
              20              25              30
Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
              35              40              45
Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
              50              55              60
Trp Pro Cys Cys Met Phe Gly
65              70

<210> 69
<211> 17
<212> PRT
<213> Conus characteristicus

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is
Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is
Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 69
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
1              5              10              15
Phe

<210> 70
<211> 232
<212> DNA
<213> Conus characteristicus

<400> 70
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccctt      60

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<210> 74
<211> 74
<212> PRT
<213> Conus circumcissus
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<400> 74

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45

Asp Lys Arg Arg Lys Cys Cys Gly Lys Asp Gly Pro Cys Pro Lys Tyr
 50 55 60

Phe Lys Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 75

<211> 23

<212> PRT

<213> Conus circumciscus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 9 and 11 is Pro or Hyp; Xaa at residue 13 is Tyr,
 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-T
 y

<400> 75

Arg Lys Cys Cys Gly Lys Asp Gly Xaa Cys Xaa Lys Xaa Phe Lys Asp
 1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
 20

<210> 76

<211> 293

<212> DNA

<213> Conus dalli

<400> 76

caagagggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60

acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120

agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180

gtgttgogat gattcggaat gcgactattc ttgctggcct tgctgtattt tatcataacc 240

tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaatgattgc agt 293

<210> 77

<211> 71

<212> PRT

<213> Conus dalli

<400> 77

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45

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100

Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
50 55 60

Trp Pro Cys Cys Ile Leu Ser
65 70

<210> 78
<211> 18
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(18)
<223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 78
Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
1 5 10 15

Leu Ser

<210> 79
<211> 299
<212> DNA
<213> Conus dalli

<400> 79
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatttgtct 60
acttctgttt ccccttactg ctgttccact ggatggagat cagcctgcag accgacctgc 120
agagcgtatg caggacggca tttcatctga acatcatcca ttttttgatt ccgtcaaaaa 180
gaaacaacag tgttgccgcg cggtggcatg caacatggga tgcgagcctt gttgtggatg 240
accagctttg ttatcgcggc tcatgaagtg tcctaataa taagtaaaac gattgcagt 299

<210> 80
<211> 72
<212> PRT
<213> Conus dalli

<400> 80
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Ser Val Lys Lys Lys Gln Gln Cys Cys Pro Pro Val Ala Cys Asn
50 55 60

Met Gly Cys Glu Pro Cys Cys Gly
65 70

<210> 81
<211> 17

<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 5, 6 and 15 is Pro or Hyp

<400> 81
Xaa Gln Cys Cys Xaa Xaa Val Ala Cys Asn Met Gly Cys Xaa Xaa Cys
1 5 10 15

Cys

<210> 82
<211> 290
<212> DNA
<213> Conus dalli

<400> 82
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgttga tcatatgtct 60
atttctgttt ccccttactg ctgttcagct caatggagat cagcctgcag accaatctgc 120
agagcgtatg caggacaaaa tttcatctga acatcatccc ttttttgatc ccgtaaacy 180
ttgttgcaac gcgggggtttt gccgcttcgg atgcacgcct tgttggttggg gaccagcttt 240
gttatcgagg cctcatcaag tgtctaata gaataaaaa tgattgcagt 290

<210> 83
<211> 69
<212> PRT
<213> Conus dalli

<400> 83
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Phe Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Gln Leu Asn Gly Asp Gln Pro Ala Asp Gln Ser
20 25 30

Ala Glu Arg Met Gln Asp Lys Ile Ser Ser Glu His His Pro Phe Phe
35 40 45

Asp Pro Val Lys Arg Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys
50 55 60

Thr Pro Cys Cys Trp
65

<210> 84
<211> 16
<212> PRT
<213> Conus dalli

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or bromo-Trp

<400> 84
Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Xaa Cys Cys Xaa
1 5 10 15

<400>	88								
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gtctgcttct	gtttcccat	actgctcttc	tgatggatgg	agatcagcct	gcagaccgac				120
ctgcagagcg	tacggaggat	gacatttcat	ctgactacat	tccctgttgc	agttggccat				180

gccccgata ctccaacggt aaacttggtt gtttttggtg ccttggtatga taatgtgttg 240
 atgaccaact ttgttatcac ggctacgtca agtgtctact gaataagtaa aatgattgca 300
 gta 303

<210> 89
 <211> 67
 <212> PRT
 <213> Conus ermineus

<400> 89
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Leu Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Thr Glu Asp Asp Ile Ser Ser Asp Tyr Ile Pro Cys Cys
 35 40 45
 Ser Trp Pro Cys Pro Arg Tyr Ser Asn Gly Lys Leu Val Cys Phe Cys
 50 55 60

Cys Leu Gly
 65

<210> 90
 <211> 20
 <212> PRT
 <213> Conus ermineus

<220>
 <221> PEPTIDE
 <222> (1)..(20)
 <223> Xaa at residue 5 and 7 is Pro or Hyp; Xaa at residue 4 is Trp or
 bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 90
 Cys Cys Ser Xaa Xaa Cys Xaa Arg Xaa Ser Asn Gly Lys Leu Val Cys
 1 5 10 15

Phe Cys Cys Leu
 20

<210> 91
 <211> 241
 <212> DNA
 <213> Conus generalis

<400> 91
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60
 actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120
 gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180
 aactttggat gccaaccttg ttgcctcacc tgataacgtg ttgatgacca actttctcga 240
 g 241

<210> 92
 <211> 70
 <212> PRT

<213> Conus generalis

<400> 92

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys
50 55 60

Gln Pro Cys Cys Leu Thr
65 70

<210> 93

<211> 16

<212> PRT

<213> Conus generalis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Pro or Hy

<400> 93

Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Leu Thr
1 5 10 15

<210> 94

<211> 241

<212> DNA

<213> Conus generalis

<400> 94

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctggttct gtttcccctt 60

actgctcttc cactggatgg agaacaacct gtagaccgac atgccgagca tatgcaggat 120

gacaattcag ctgcacagaa cccctgggtt attgccatca gacagtgttg cacgttctgc 180

aactttggat gccagccttg ttgcgtcccc tgataacgtg ttgatgacca actttctcga 240

g 241

<210> 95

<211> 70

<212> PRT

<213> Conus generalis

<400> 95

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Glu Gln Pro Val Asp
20 25 30

Arg His Ala Glu His Met Gln Asp Asp Asn Ser Ala Ala Gln Asn Pro
35 40 45

Trp Val Ile Ala Ile Arg Gln Cys Cys Thr Phe Cys Asn Phe Gly Cys

50

55

60

Gln Pro Cys Cys Val Pro
65 70

<210> 96
<211> 16
<212> PRT
<213> *Conus generalis*

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 96
Xaa Cys Cys Thr Phe Cys Asn Phe Gly Cys Gln Xaa Cys Cys Val Xaa
1 5 10 15

<210> 97
<211> 862
<212> DNA
<213> *Conus geographus*

<400> 97
gtcgactcta gaggatccga caacaaagag tcaacccac tgccacgtca agagcgaagc 60
gccacagcta agacaagagg gatcgatagc agttcatgat gtctaaactg ggagtcttgt 120
tgaccatctg tctgcttctg tttccctta ctgctcttcc gatggatgga gatgaacctg 180
caaaccgacc tgtcgagcgt atgcaggaca acatttcac tgagcagtat cccttggttg 240
agaagagacg agattgttgc actccgccga agaaatgcaa agaccgacaa tgcaaaccac 300
agagatgttg cgctggacga taacgtgttg atgaccaact ttatcacggc tacgtcaagt 360
gtttagttaa taagtaaaat gattgcagtc ttgctcagat ttgcttttgt gtttttgtct 420
aaagatcaat gaccaaaccg ttgttttgat gcggtattgtc atatatttct cgattccaat 480
ccaacactag atgatttaat cacgatagat taattttcta tcaatgcctt gatttttcgt 540
ctgtcatatc agttttgttt atattttatt tttcgtcact gtctacacaa acgcatgcat 600
gcacgcatgc acgcacacac gcacgcagc tcgcacaaac atgcgcgcgc acgcacacac 660
acacacacac acacaaacac acacacaagc aatcacacaa ttattgacat tattttattta 720
ttcattgatg tatttggtat tcgtttgctt gtttttagaa tagtttgagg cgtctttttt 780
ggatttattt gaactgcttt attgtatacg agtacttcgt gctttgaaac actgctgaaa 840
ataaaacaaa cactgacgta gc 862

<210> 98
<211> 75
<212> PRT
<213> *Conus geographus*

<400> 98
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

<400>	100						
ggccagacga	caacaaagag	tcaaccccac	tgccacgtca	agagcgaagc	gccacagcta		60
agacaagagg	gatcgatagc	agttcatgat	gtctaaactg	ggagtcttgt	tgaccatctg		120
tctgcttctg	tttcccctta	ctgctcttcc	gatggatgga	gatgaacctg	caaaccgacc		180
tgtcgagcgt	atgcaggaca	acatttcac	tgagcagtat	cccttgtttg	agaagagacg		240
agattgtttg	actccgccga	ggaaatgcaa	agaccgacga	tgcaaacc	tgaaatgttg		300
cgctggacga	taacgtgttg	atgaccaact	ttatcacggc	tagctcagtg	tttagtgaat		360
aagtaaaatg	attgcagtct	tgctcagatt	gcttttgtgt	tttggcttaa	gatcaatgac		420
caaaccgttg	ttttgatgcg	gattgtcata	tattttctga	ttccaatcca	acactagatg		480
atttaatcac	gatagattaa	ttttctatca	atgccttgat	ttttcgtctg	tcatatcagt		540
tttgtttata	tttatttttt	cgtcactgtc	tacacaaacg	catgcatgca	cgcattgcacg		600
cacacacgca	cgcacgctcg	cacaaacatg	cgcgcgcacg	cacacacaca	cacacacaca		660
aacacacaca	cgaagcaatc	acacaattag	ttgacattat	ttattttattc	attgatgtat		720
ttgttattcg	tttgcttggt	tttagaatag	tttgaggccg	tctttttgga	tttattttgaa		780
ctgctttatt	gtatacgagt	acttcgtgct	ttgaaacact	gctgaaaata	aaacaaacac		840
tqacqtaqca	aaaaaaaaaa						860

<210> 101
 <211> 75
 <212> PRT
 <213> Conus geographus

<400> 101
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
 35 40 45
 Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Arg Cys Lys Pro Met Lys Cys Cys Ala Gly Arg
 65 70 75

<210> 102
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 102
 Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Met Lys Cys Cys Ala
 20

<210> 103
 <211> 22
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 7 and 17 is Pro or Hyp

<400> 103
 Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Arg Cys Lys
 1 5 10 15
 Xaa Leu Lys Cys Cys Ala
 20

<210> 104
 <211> 321
 <212> DNA
 <213> Conus gloriamaris

<400> 104
 ctactatag gaattcgagc tcggtacacg ggatcgatag cagttcatga tgtctaaact 60
 gggagccttg ttgaccatct gtctacttct gttttcccta actgctgttc cgctggatgg 120

agatcaacat gcagaccaac ctgcagagcg tctgcatgac cgccttccaa ctgaaaatca 180
 tcccttatat gatcccgta aacgggtgtg cgatgattcg gaatgcgact attcttgctg 240
 gccttgctgt atgtttggat aacctttggt atcgcgggcct cgataagtgt ctaatgaata 300
 agtaaaacga ttgcagtagg c 321

<210> 105
 <211> 71
 <212> PRT
 <213> Conus gloriamaris

<400> 105
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
 50 55 60
 Trp Pro Cys Cys Met Phe Gly
 65 70

<210> 106
 <211> 17
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue is 6 Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 106
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Met
 1 5 10 15

Phe

<210> 107
 <211> 257
 <212> DNA
 <213> Conus gloriamaris

<400> 107
 gttcatgatg tctaaactgg gagtcttggt gatcatctgt ctacttctgt ttccccttac 60
 tgctgttccg ctggatggag atcaacctgc agaccgatat gcagagcgta tgcaggacga 120
 catttcatct gaacatcatc ccattgttga tgccgtcaga ggggtgttgcc atctgttggc 180
 atgcccgttc ggatgctcgc cttgttggtg gtgatcagct ttgttatcgc ggcctcatca 240
 agtgactcta atgcaaa 257
 <210> 108
 <211> 69

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<400>      108
Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Phe
1          5          10          15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Tyr
          20          25          30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu His His Pro Met Phe
          35          40          45

Asp Ala Val Arg Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
          50          55          60

Ser Pro Cys Cys Trp
65

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<210> 109
<211> 17
<212> PRT
<213> Conus gloriamaris

<220>
<221> PEPTIDE
<222> (1)..(17)
<223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 17 is Trp or brom
o-Tr
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<400> 109
Gly Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys
1 5 10 15

Xaa

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<210> 110
<211> 471
<212> DNA
<213> Conus gloriamaris
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<400>	110						
gagacgacaa	ggaacagtca	acccacacagc	cacgccaaga	gcagacagcc	acagctacgt		60
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ggtactgttt	cccctggcaa	cgctccagct	ggatgcagat	caacctgtag	aacgatatgc		180
ggagaacaaa	cagctcctca	accagatga	aaggagggaa	atcatattgc	atgctctggg		240
gacgcgatgc	tgttcttggg	atgtgtgcga	ccaccogagt	tgtacttgct	gcggcggtta		300
gcgccgaaca	tccatggcgc	tgtgctgggc	ggttttatcc	aacaacgaca	gcgtttgttg		360
atttcatgta	tcattgcgcc	cacgtctctt	gtctaagaat	gacgaacatg	attgcactct		420
ggttcagatt	tcgtgttctt	ttctgacaat	aaatgacaaa	actccaaaaa	a		471

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<210> 111
<211> 71
<212> PRT
<213> Conus gloriamaris
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<400> 111
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro

1 5 10 15
 Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
 20 25 30
 Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Ile Leu
 35 40 45
 His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
 50 55 60
 Ser Cys Thr Cys Cys Gly Gly
 65 70

<210> 112
 <211> 16
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
 -Tr

<400> 112
 Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys Gly
 1 5 10 15

<210> 113
 <211> 304
 <212> DNA
 <213> Conus laterculatus

<400> 113
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgctct tccgatggat ggagatcaac ctgcagaccg 120
 acctgcagag cgtatgcagg acgtttcatc tgaacagcat cccttgatg atcccgtaa 180
 acggtgttgc gactggccat gcagcggatg catcccttgt tgctaatagt aacaacgtgt 240
 tgataaccaa ctttcttacc acgactacgt caagtgtcta atgaataagt aaaatgattg 300
 cagt 304

<210> 114
 <211> 65
 <212> PRT
 <213> Conus laterculatus

<400> 114
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Val Ser Ser Glu Gln His Pro Leu Tyr Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Gly Cys Ile Pro Cys
 50 55 60

Cys

65

<210> 115
 <211> 13
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 5 and 11 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp

<400> 115
 Cys Cys Asp Xaa Xaa Cys Ser Gly Cys Ile Xaa Cys Cys
 1 5 10

<210> 116
 <211> 313
 <212> DNA
 <213> Conus laterculatus

<400> 116
 cgacctcaag aaggatcgat agcagttcat gatgtctaaa ctgggagtct tgttgaccat 60
 ctgtctgctt ctgtttcccc ttactgtctt ggatggagat caacctgcag accgacttgc 120
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgaaaaga gacgagactg 180
 ttgcacacct ccgaagaaat gcagagaccg acaatgcaaa cctgcacgtt gttgcggagg 240
 ataacgtgtt gatgaccaac ttgtttatca cggctacgtc aagtgtctag tgaataagta 300
 aaacgattgc agt 313

<210> 117
 <211> 71
 <212> PRT
 <213> Conus laterculatus

<400> 117
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Asp Gly Asp Gln Pro Ala Asp Arg Leu Ala Glu
 20 25 30
 Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Glu Lys Arg
 35 40 45
 Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
 50 55 60
 Pro Ala Arg Cys Cys Gly Gly
 65 70

<210> 118
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 6, 17 and 17 is Pro or Hyp

116
 313
 DNA
 Conus laterculatus

<400> 118

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Arg Asp Arg Gln Cys Lys
 1 5 10 15

Xaa Ala Arg Cys Cys Gly
 20

<210> 119

<211> 314

<212> DNA

<213> Conus laterculatus

<400> 119

gggatcgata gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctgcttc 60
 tgtttcccct tactgctctt ccgatggatg gagatcaact tgcacgccga tctgcagagc 120
 gtatgcagga caacatttca tctgagcagc atcacctctt tgaaaagaga cgaccacat 180
 gttgcaccta tgacgggagt tgcctaaaag aatcatgcat gcgtaaagct tgttgccgat 240
 gataacgtgt tgatgaccaa ctttgttatc acggctactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 120

<211> 74

<212> PRT

<213> Conus laterculatus

<400> 120

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Ser
 20 25 30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His His Leu Phe
 35 40 45

Glu Lys Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60

Glu Ser Cys Met Arg Lys Ala Cys Cys Gly
 65 70

<210> 121

<211> 22

<212> PRT

<213> Conus laterculatus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 121

Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15

Met Arg Lys Ala Cys Cys
 20

<210> 122
 <211> 314
 <212> DNA
 <213> Conus laterculatus

<400> 122
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 gtatgcagga caacatttca tctgagcagc atcccttctt tgaaaggaga cgaccaccat 180
 gttgcaccta tgacgggagt tgccataaag aatcatgcaa gcgtaaagct tgttgcggat 240
 aataacgtgt tgatgaccaa ctttggtatc acggctactc aagtgtctaa tgaataagta 300
 aaatgattgc agta 314

<210> 123
 <211> 74
 <212> PRT
 <213> Conus laterculatus

<400> 123
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Thr Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Leu Ala Arg Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Arg Arg Arg Pro Pro Cys Cys Thr Tyr Asp Gly Ser Cys Leu Lys
 50 55 60
 Glu Ser Cys Lys Arg Lys Ala Cys Cys Gly
 65 70

<210> 124
 <211> 22
 <212> PRT
 <213> Conus laterculatus

<220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 2 and 3 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 124
 Arg Xaa Xaa Cys Cys Thr Xaa Asp Gly Ser Cys Leu Lys Xaa Ser Cys
 1 5 10 15
 Lys Arg Lys Ala Cys Cys
 20

<210> 125
 <211> 247
 <212> DNA
 <213> Conus leopardus

<400> 125

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60
 actgctcttc ggctgggttg agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
 gacattccag atggacagca tccgttaaatt gataggcaga taaactgttg cccgtggcca 180
 tgccctagta catgccgcca tcaatgctgc cattaatgat aacgtgttga tgaccaactt 240
 tctcgag 247

<210> 126
 <211> 71
 <212> PRT
 <213> Conus leopardus

<400> 126
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Gly Asp Gln Pro Ala Glu
 20 25 30
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asp Gly Gln His Pro
 35 40 45
 Leu Asn Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Ser Thr
 50 55 60
 Cys Arg His Gln Cys Cys His
 65 70

<210> 127
 <211> 19
 <212> PRT
 <213> Conus leopardus

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp

<400> 127
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Ser Thr Cys Arg His Gln
 1 5 10 15

Cys Cys His

<210> 128
 <211> 244
 <212> DNA
 <213> Conus lividus

<400> 128
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 actgctcttc ggctgggttag agatcaacct gcagagcgac ctgcaaagcg tacgcaggac 120
 gacattccaa atggacagga tccgttaatt gataggcaga taaattgttg cccttgcca 180
 tgccctgatt catgccacta tcaatgctgc cactgataac gtgttgatga ccaactttct 240
 cgag 244

<210> 129

<211> 71
 <212> PRT
 <213> *Conus lividus*

<400> 129
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Arg Leu Val Arg Asp Gln Pro Ala Glu
 20 25 30
 Arg Pro Ala Lys Arg Thr Gln Asp Asp Ile Pro Asn Gly Gln Asp Pro
 35 40 45
 Leu Ile Asp Arg Gln Ile Asn Cys Cys Pro Trp Pro Cys Pro Asp Ser
 50 55 60
 Cys His Tyr Gln Cys Cys His
 65 70

<210> 130
 <211> 19
 <212> PRT
 <213> *Conus lividus*

<220>
 <221> PEPTIDE
 <222> (1)..(19)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6, 8 and 10 is Pro or Hyp; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 15 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 130
 Xaa Ile Asn Cys Cys Xaa Xaa Xaa Cys Xaa Asp Ser Cys His Xaa Gln
 1 5 10 15

Cys Cys His

<210> 131
 <211> 275
 <212> DNA
 <213> *Conus lynceus*

<400> 131
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 ctgtttcccc ttactgctct tccgatggat ggagatcaat ctgcagaccg acttgacagag 120
 cgtatgcagg acaacatttc atctgagcag catcccttct ttgaaaagag aggacgagac 180
 tgttgacacac ctccgaggaa atgcagagac cgagcctgca aacctcaacg ttgttgcgga 240
 ggataagctg ttgatgacca actttgttat acggc 275

<210> 132
 <211> 75
 <212> PRT
 <213> *Conus lynceus*

<400> 132
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Ser Ala Asp Arg Leu

20

25

30

Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45

Glu Lys Arg Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp
 50 55 60

Arg Ala Cys Lys Pro Gln Arg Cys Cys Gly Gly
 65 70 75

<210> 133
 <211> 23
 <212> PRT
 <213> Conus lynceus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 7, 8 and 18 is Pro or Hyp

<400> 133
 Gly Arg Asp Cys Cys Thr Xaa Xaa Arg Lys Cys Arg Asp Arg Ala Cys
 1 5 10 15

Lys Xaa Gln Arg Cys Cys Gly
 20

<210> 134
 <211> 803
 <212> DNA
 <213> Conus magus

<400> 134
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 gcttctgttt ccccttactg ctcttccgat ggatggagat gaacctgcaa accgacctgt 120
 cgagcgtatg caggacaaca tttcatctga gcagtatccc ttgtttgaga agagacgaga 180
 ttgttgact cgcgcaaga aatgcaaaga ccgacaatgc aaaccccgaga gatgttgccg 240
 tggacgataa cgtgttgatg accaacttta tcacggctac gtcaagtgtt tagtgaataa 300
 gtaaaatgat tgcagtcttg ctgagatttg cttttgtgtt ttggtctaaa gatcaatgac 360
 caaaccgttg ttttgatgcg gattgtcata ttttctcga ttccaatcca aactagatg 420
 atttaatcac gatagattaa ttttctatca atgccttgat ttttctctg tcatatcagt 480
 tttgtttata tttatTTTTT cgtcactgtc tacacaaacg catgcatgca cgcattgcacg 540
 cacacacgca cgcacgctcg cacaacatg cgcgcgcacg cacacacaca cacacacaca 600
 caaacacaca cacgaagcaa tcacacaatt agttgacatt atttatttat tcattgatgt 660
 atttgttatt cgtttgcttg tttttagaat agtttgaggc ^gtctttttg gatttatttg 720
 aactgcttta ttgtatacga gtacttcgtg cggggaaaca ctgctgaaaa taaaacaaac 780
 actgacgtag caaaaaaaaaaaa aaa 803

<210> 135
 <211> 75
 <212> PRT

134-135-136-137-138-139-140-141-142-143-144-145-146-147-148-149-150-151-152-153-154-155-156-157-158-159-160-161-162-163-164-165-166-167-168-169-170-171-172-173-174-175-176-177-178-179-180-181-182-183-184-185-186-187-188-189-190-191-192-193-194-195-196-197-198-199-200-201-202-203-204-205-206-207-208-209-210-211-212-213-214-215-216-217-218-219-220-221-222-223-224-225-226-227-228-229-230-231-232-233-234-235-236-237-238-239-240-241-242-243-244-245-246-247-248-249-250-251-252-253-254-255-256-257-258-259-260-261-262-263-264-265-266-267-268-269-270-271-272-273-274-275-276-277-278-279-280-281-282-283-284-285-286-287-288-289-290-291-292-293-294-295-296-297-298-299-300-301-302-303-304-305-306-307-308-309-310-311-312-313-314-315-316-317-318-319-320-321-322-323-324-325-326-327-328-329-330-331-332-333-334-335-336-337-338-339-340-341-342-343-344-345-346-347-348-349-350-351-352-353-354-355-356-357-358-359-360-361-362-363-364-365-366-367-368-369-370-371-372-373-374-375-376-377-378-379-380-381-382-383-384-385-386-387-388-389-390-391-392-393-394-395-396-397-398-399-400-401-402-403-404-405-406-407-408-409-410-411-412-413-414-415-416-417-418-419-420-421-422-423-424-425-426-427-428-429-430-431-432-433-434-435-436-437-438-439-440-441-442-443-444-445-446-447-448-449-450-451-452-453-454-455-456-457-458-459-460-461-462-463-464-465-466-467-468-469-470-471-472-473-474-475-476-477-478-479-480-481-482-483-484-485-486-487-488-489-490-491-492-493-494-495-496-497-498-499-500-501-502-503-504-505-506-507-508-509-510-511-512-513-514-515-516-517-518-519-520-521-522-523-524-525-526-527-528-529-530-531-532-533-534-535-536-537-538-539-540-541-542-543-544-545-546-547-548-549-550-551-552-553-554-555-556-557-558-559-560-561-562-563-564-565-566-567-568-569-570-571-572-573-574-575-576-577-578-579-580-581-582-583-584-585-586-587-588-589-590-591-592-593-594-595-596-597-598-599-600-601-602-603-604-605-606-607-608-609-610-611-612-613-614-615-616-617-618-619-620-621-622-623-624-625-626-627-628-629-630-631-632-633-634-635-636-637-638-639-640-641-642-643-644-645-646-647-648-649-650-651-652-653-654-655-656-657-658-659-660-661-662-663-664-665-666-667-668-669-670-671-672-673-674-675-676-677-678-679-680-681-682-683-684-685-686-687-688-689-690-691-692-693-694-695-696-697-698-699-700-701-702-703-704-705-706-707-708-709-710-711-712-713-714-715-716-717-718-719-720-721-722-723-724-725-726-727-728-729-730-731-732-733-734-735-736-737-738-739-740-741-742-743-744-745-746-747-748-749-750-751-752-753-754-755-756-757-758-759-760-761-762-763-764-765-766-767-768-769-770-771-772-773-774-775-776-777-778-779-780-781-782-783-784-785-786-787-788-789-790-791-792-793-794-795-796-797-798-799-800-801-802-803-804-805-806-807-808-809-810-811-812-813-814-815-816-817-818-819-820-821-822-823-824-825-826-827-828-829-830-831-832-833-834-835-836-837-838-839-840-841-842-843-844-845-846-847-848-849-850-851-852-853-854-855-856-857-858-859-860-861-862-863-864-865-866-867-868-869-870-871-872-873-874-875-876-877-878-879-880-881-882-883-884-885-886-887-888-889-890-891-892-893-894-895-896-897-898-899-900-901-902-903-904-905-906-907-908-909-910-911-912-913-914-915-916-917-918-919-920-921-922-923-924-925-926-927-928-929-930-931-932-933-934-935-936-937-938-939-940-941-942-943-944-945-946-947-948-949-950-951-952-953-954-955-956-957-958-959-960-961-962-963-964-965-966-967-968-969-970-971-972-973-974-975-976-977-978-979-980-981-982-983-984-985-986-987-988-989-990-991-992-993-994-995-996-997-998-999-1000

<400> 135

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Glu Pro Ala Asn Arg Pro
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Glu Lys Arg Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg
50 55 60

Gln Cys Lys Pro Gln Arg Cys Cys Ala Gly Arg
65 70 75

<210> 136

<211> 22

<212> PRT

<213> Conus magus

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<221> PEPTIDE

<222> (1) . . (22)

<223> Xaa at residue 6 and 7 is Pro or Hyp

<400> 136

Arg Asp Cys Cys Thr Xaa Xaa Lys Lys Cys Lys Asp Arg Gln Cys Lys
1 5 10 15

Xaa Gln Arg Cys Cys Ala
20

<210> 137

<211> 656

<212> DNA

<213> Conus magus

<400> 137

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gcttctgttt ccccttactg ctcttccaat ggatggagat caacctgcag accaacctgc 120

agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata tqagaaaaaaq 180

gtgttgcggc cccggcggtt catgccccgt atatttcaga gacaatttta tttgtggttg 240

ttgttaaattg acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300

tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatTTTtG gtctaaagat 360

caatgaccaa accgttgttt tgggtgtggat tttcatatat ttctcgagtc ctatccaaca 420

ctagatgatt taatcacgat agatctgatt tttttatcaa aggcttggtt tttcgtctgt 480

cacatcagtt ttgtttatat ttaatTTTTc gtcactgatt acacacacgc atgaacgcac 540.

agagtactaa cacatacaca cacacacaca cacacacaca cacacacaca cacacacaca 600

cacacacaca cacgcgcgcg cgcgggcgcca tctagtagcg ccgcgacgac acacac 656

<210> 138

<211> 74

<212> PRT

<213> Conus magus

<400> 138

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Met Arg Lys Arg Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 139

<211> 21

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(21)

<223> Xaa at residue 4 and 9 is Pro or Hyp; Xaa at residue is 11 Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 139

Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp Asn Phe
1 5 10 15

Ile Cys Gly Cys Cys
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<210> 140

<211> 594

<212> DNA

<213> Conus magus

<400> 140

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agagcgtatg caggacgaca tttcatctga gctgcatccc ttgtcaatca gaaaaagaat	180
gtgttgccgc gagagtgcgc catgccccag ctatttcaga aacagtcaga tttgtcattg	240
ttgttaaagt acaacgtgtc gatgaccacc ttcgttatca cgactaatga taagtaaaat	300
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ttgttttgat gtggattttc atatatttct cgagtcctat ccaacactag atgatttaat	420
cacgatagat ctgatttttt tatcaaagcc ttgggttttc gtctgtcaca tcagttttgt	480
ttatatttaa tttttcgtca ctgattacac acacgcatga acgcacagac gtactaacac	540
atacacacac acacacacac acacacacac acacacacac acacacacac acac	594

<210> 141

<211> 74

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100

<212> PRT
 <213> Conus magus

<400> 141
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Arg Asp Gly Asp Gln Ser Val Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Leu His Pro Leu Ser
 35 40 45
 Ile Arg Lys Arg Met Cys Cys Gly Glu Ser Ala Pro Cys Pro Ser Tyr
 50 55 60
 Phe Arg Asn Ser Gln Ile Cys His Cys Cys
 65 70

<210> 142
 <211> 22
 <212> PRT
 <213> Conus magus
 <220>
 <221> PEPTIDE
 <222> (1)..(22)
 <223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 142
 Met Cys Cys Gly Xaa Ser Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 143
 <211> 501
 <212> DNA
 <213> Conus magus

<400> 143
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 agatcgtatg caggacgaca tttcatctga gcagtatccc ttgtttgata agagacaaaa 180
 gtgttgccgc cccggcgggt catgccccgt atatttcaca gacaatttta tttgtggttg 240
 ttgttaaagt acaacgtgtc gatgaccaac ttcattatca cgactacgcc aagtgtctaa 300
 tgaataaata aaatgattgc agtctcgctc agatttgctt ttgtatttgg tctaaagatc 360
 aatgacaaaa ccgttggttt ggtgctggat tttcaatat ttctcgattc ctatccaaca 420
 ctagatgatt taatcacgat agatctgatt ttttatcaa tgccttaatt ttttgctctg 480
 tcatatcagt tttgtttata t 501

<210> 144
 <211> 74
 <212> PRT

<400> 144

Phe Thr Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<213> Conus magus

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

Asn Phe Ile Cys Gly Cys Cys
20

<213> Conus magus

ctagatgatt taatcacgat agatctgatt tttt 454

<213> Conus magus

<400> 147

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe
35 40 45

Asp Lys Arg Gln Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr
50 55 60

Phe Arg Asp Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 148

<211> 23

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 148

Xaa Lys Cys Cys Gly Xaa Gly Gly Ser Cys Xaa Val Xaa Phe Arg Asp
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 149

<211> 22

<212> PRT

<213> Conus magus

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 10 and 20 is
Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 149

Xaa Lys Cys Cys Ser Gly Gly Ser Cys Xaa Leu Xaa Phe Arg Asp Arg
1 5 10 15

Leu Ile Cys Xaa Cys Cys
20

<210> 150

<211> 19

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Xaa at residue 16 is Pro or Hyp

<400> 150

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

Cys Cys Asn

<210> 151

<211> 321

<212> DNA

<213> Conus marmoreus

<400> 151

caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60

gcttctgttt cccgttactg ctcttccgat ggatgggtgat caacctgcag accgacttgt 120

agagcgtatg caggacaaca tttcatctga gcagcatccc ttctttgaaa agagaagagg 180

aggctgttgc acacctccga ggaaatgcaa agaccgagcc tgcaaacctg cacgttgctg 240

cggcccagga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300

gaataagtaa aacgattgca g 321

<210> 152

<211> 76

<212> PRT

<213> Conus marmoreus

<400> 152

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 153

<211> 24

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 3, 8, 18 and 24 is Pro or Hyp

<400> 153

Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 154

<211> 296

<212> DNA

<213> Conus marmoreus

<400> 154

gagctcggtta ccccgacctc aagagggatc gatagcagtt catgatgtct aaactgggaa 60

P00001-00001

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<210> 155
<211> 68
<212> PRT
<213> Conus marmoreus
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<210> 156
<211> 14
<212> PRT
<213> Conus marmoreus
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<220>
<221>  PEPTIDE
<222>  (1)..(14)
<223>  Xaa at residue 12 is Pro or Hyp
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<210>	157
<211>	355
<212>	DNA
<213>	Conus marmoreus

<210>	158
<211>	69
<212>	PRT

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Phe Phe Asp Arg
35 40 45

<220>

<221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 5 and 7 is Pro or Hyp

<400> 165
 Met Gly Cys Cys Xaa Phe Xaa Cys Lys Thr Ser Cys Thr Thr Leu Cys
 1 5 10 15

Cys

<210> 166
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Trp or bromo-Trp

<400> 166
 Cys Cys His Xaa Asn Xaa Cys Asp His Leu Cys Ser Cys Cys Gly Ser
 1 5 10 15

<210> 167
 <211> 357
 <212> DNA
 <213> Conus marmoreus

<400> 167
 gccaaagcttg catgcctgca ggatgactct agaggatccc cacctcaaga gggatcgata 60
 gcagttcatg atgtctaaac tgggagtctt gttgaccatc tgtctacttc tgtttgcct 120
 tactgctgtt ccgctggatg gagatcaacc tgcagaccga cctgcagaac gtatgcagga 180
 cgacatttca tctgaacgtc atcccatggt tgatgccgtc agagattggt gcccggtgcc 240
 ggcattgcccc tttggatgca acccttggtg tggatgacca gctttgttat cgggacctca 300
 tcaagtgtct aatgaataag taaaaaacga ttcgagtggg taccgagctc gaattcc 357

<210> 168
 <211> 67
 <212> PRT
 <213> Conus marmoreus

<400> 168
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Ala Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser His Pro Met Phe Asp Ala
 35 40 45

Val Arg Asp Cys Cys Pro Leu Pro Ala Cys Pro Phe Gly Cys Asn Pro
 50 55 60

Cys Cys Gly
 65

<210> 169
 <211> 16

Val

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<400> 174
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60
actgctcttc cgctggatga agatcaaccg gtacaccgac ctgcagagcg tatgcaggac 120
atttcacctg atcaacatct cttctttgat ctcatcaaac ggtgctgcga gttgccatgc 180
gggccaggct tttgcgtccc ttgttgctga catcaataac gtgttgatga ccaactttct 240
cgaq 244

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<400> 175
Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Arg Pro Ala Glu Arg Met Gln Asp Ile Ser Ser Asp Gln His Leu Phe
35 40 45

Cys Val Pro Cys Cys
65

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<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 5, 8
      adn 13 is Pro or Hy
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<210>	177
<211>	262
<212>	DNA
<213>	Conus nobilis

<400> 177
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctacttct gtttcccctt 60

actgcttttc cgatggatgg agatcaacct gcagaccaac ctgcagatcg tatgcaggac 120
 gacatttcat ctgagcagta tcccttggtt gataagagac aaaagtgttg cactgggaag 180
 aaggggtcat gctccggcaa agcatgcaaa aatctcaa atgttgctctgg acgataacgt 240
 gttgatgacc aactttctcg ag 262

<210> 178
 <211> 78
 <212> PRT
 <213> Conus nobilis

<400> 178
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Phe Pro Met Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Gln Pro Ala Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro
 35 40 45
 Leu Phe Asp Lys Arg Gln Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys
 50 55 60
 Ser Gly Lys Ala Cys Lys Asn Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 179
 <211> 23
 <212> PRT
 <213> Conus nobilis

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 179
 Xaa Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Asn Leu Lys Cys Cys Ser
 20

<210> 180
 <211> 238
 <212> DNA
 <213> Conus pulicarius

<400> 180
 ggatccatga tgtctaaact gggagtgttg ttgaccatct gtctgcttct gtttcccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttctttgat cccgtcaaac ggtgttgcaa cagctgttac 180
 atgggatgca tcccttggtg cttctagtaa taacgtgttg atgaccaact ttctcgag 238

<210> 181
 <211> 68
 <212> PRT
 <213> Conus pulicarius

<400> 181

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Phe
35 40 45

Phe Asp Pro Val Lys Arg Cys Cys Asn Ser Cys Tyr Met Gly Cys Ile
50 55 60

Pro Cys Cys Phe
65

<210> 182

<211> 14

<212> PRT

<213> Conus pulicarius

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 5 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 182

Cys Cys Asn Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10

<210> 183

<211> 238

<212> DNA

<213> Conus quercinus

<400> 183

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60

acagctcttc agctggatgg agatcaacct gcagaccgac ctgcagagcg tacgcaggac 120

attgcatctg aacagtatcg aaagtttgat cagagacaga ggtgttgcca gtggccatgc 180

cccggtagtt gcagatgctg ccgtactggt taacgtgttg atgaccaact ttctcgag 238

<210> 184

<211> 70

<212> PRT

<213> Conus quercinus

<400> 184

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Thr Gln Asp Ile Ala Ser Glu Gln Tyr Arg Lys
35 40 45

Phe Asp Gln Arg Gln Arg Cys Cys Gln Trp Pro Cys Pro Gly Ser Cys
50 55 60

Arg Cys Cys Arg Thr Gly
65 70

181
182
183
184

<210> 185
 <211> 17
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 7 and 9 is Pr
 o or Hyp; Xaa at residue 6 is Trp or bromo-Tr

<400> 185
 Xaa Arg Cys Cys Gln Xaa Xaa Cys Xaa Gly Ser Cys Arg Cys Cys Arg
 1 5 10 15

Thr

<210> 186
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 and 14 is Pro or Hyp

<400> 186
 Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 187
 <211> 15
 <212> PRT
 <213> Conus quercinus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 11 14 is Pro or Hyp; Xaa at residue 7 is Trp or br
 omo-Tr

<400> 187
 Cys Cys Ser Arg His Cys Xaa Val Cys Ile Xaa Cys Cys Xaa Asn
 1 5 10 15

<210> 188
 <211> 323
 <212> DNA
 <213> Conus radiatus

<400> 188
 tcaagaagga tcgatagcag ttcgatgatgt ctaaactggg agtcttggtg accatctgtc 60
 tgcttctggt tccccttact gctcttccga tggatggaga tcaacctgta gaccgacttg 120
 cagagcgtat gcaggacaac atttcatctg agcag .cac cttctttgaa aagagactac 180
 catcgtggtg ctcccttaac ttgcggcttt gccagtagc agcatgcaaa cgtaaccctt 240
 gttgcacagg ataacgtggt gatgaccaac tttgttatca cggctacgtc aagtgtctag 300
 tgaataagta aaacgattgc agt 323

<210> 189
 <211> 76
 <212> PRT
 <213> Conus radiatus

<400> 189
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Val Asp Arg Leu
 20 25 30
 Ala Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Thr Phe Phe
 35 40 45
 Glu Lys Arg Leu Pro Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Pro
 50 55 60
 Val Pro Ala Cys Lys Arg Asn Pro Cys Cys Thr Gly
 65 70 75

<210> 190
 <211> 24
 <212> PRT
 <213> Conus radiatus
 <220>
 <221> PEPTIDE
 <222> (1)..(24)
 <223> Xaa at residue 2, 13, 15 and 21 is Pro or Hyp

<400> 190
 Leu Xaa Ser Cys Cys Ser Leu Asn Leu Arg Leu Cys Xaa Val Xaa Ala
 1 5 10 15
 Cys Lys Arg Asn Xaa Cys Cys Thr
 20

<210> 191
 <211> 336
 <212> DNA
 <213> Conus radiatus

<400> 191
 aggtcgactc tagaggatcc ccaaggatcg atagcagttc atgatgtcta aactgggagt 60
 cttgttgacc atctgtctgc ttctgtttcc ccttactgct cttccgatgg atggagatca 120
 acctgcagac cgacttgacg agcgtatgca ggacgacatt tcatctgagc agcatccctt 180
 ctttaaaaag agacaacaaa gatgttgac cgттаagagg atttgtccag taccagcatg 240
 cagaagtaaa ccttggtgca aatcataacg tattgatgac caactttggt atcacggcta 300
 cgtcaagtgt ctagtgaata agtaaaatga ttgcag 336

<210> 192
 <211> 75
 <212> PRT
 <213> Conus radiatus

<400> 192
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Lys Lys Arg Gln Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Pro Val
50 55 60

Pro Ala Cys Arg Ser Lys Pro Cys Cys Lys Ser
65 70 75

<210> 193

<211> 24

<212> PRT

<213> Conus radiatus

<220>

<221> PEPTIDE

<222> (1)..(24)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12, 14 and 20
is Pro or Hy

<400> 193

Xaa Gln Arg Cys Cys Thr Val Lys Arg Ile Cys Xaa Val Xaa Ala Cys
1 5 10 15

Arg Ser Lys Xaa Cys Cys Lys Ser
20

<210> 194

<211> 326

<212> DNA

<213> Conus radiatus

<400> 194

acctcaagaa ggatcgatag cagttcatga tgtctaaact gggagtcttg ttgaccatct 60

gtctgcttct gtttcccgtt actgctcttc cgatggatgg tgatcaacct gcagaccgac 120

ttgtagagcg tatgcaggac aacatttcac ctgagcagca tcccttcttt gaaaagagaa 180

gaggaggctg ttgcacacct ccgaggaaat gcaaagaccg agcctgcaaa cctgcacggt 240

gctgcggccc aggataacgt gttgatgacc aactttgtta tcacggctac gtcaagtgtc 300

tagtgaataa gtaaaacgat tgcagt 326

<210> 195

<211> 76

<212> PRT

<213> Conus radiatus

<400> 195

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Val Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
20 25 30

Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
35 40 45

Glu Lys Arg Arg Gly Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp
50 55 60

Arg Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
65 70 75

<210> 196
<211> 24
<212> PRT
<213> Conus radiatus

<220>
<221> PEPTIDE
<222> (1)..(24)
<223> Xaa at residue 7, 8, 18 and 24 is Pro or Hyp

<400> 196
Arg Gly Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys
1 5 10 15

Lys Xaa Ala Arg Cys Cys Gly Xaa
20

<210> 197
<211> 238
<212> DNA
<213> Conus rattus

<400> 197
ggatccatga tgtctaaact gggagtcttg gtgaccatct gcctgcttct gttccctctt 60
gctgcttttc cactggatgg agatcaacct gcagaccacc ctgcaaagcg tacgcaagat 120
gacagttcag ctgccctgat caatgcctgg cttgatgaat cccagacttg ctgcagtaac 180
tgcggtgaag attgtgatgg ttgttgccag taacgtgttg atgaccaact ttctcgag 238

<210> 198
<211> 70
<212> PRT
<213> Conus rattus

<400> 198
Gly Ser Met Met Ser Lys Leu Gly Val Leu Val Thr Ile Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Ala Ala Phe Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

His Pro Ala Lys Arg Thr Gln Asp Asp Ser Ser Ala Ala Leu Ile Asn
35 40 45

Ala Trp Leu Asp Glu Ser Gln Thr Cys Cys Ser Asn Cys Gly Glu Asp
50 55 60

Cys Asp Gly Cys Cys Gln
65 70

<210> 199
<211> 16
<212> PRT
<213> Conus rattus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 9 is Glu or gamma-carboxy Gl

196
238
70
198
16
199

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<210> 203
<211> 316
<212> DNA
<213> Conus stercusmuscarum
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<400> 203
 gatcgatagc agttcgtgat gtctaaactg ggagtccttgt tgaccatctg tctgcttctg 60
 tttcccttta ctgctcttcc gatggatgga gatcaacctg cagaccaacc tgcagatcgt 120
 atgcagaacg acatttcatac tgagcagtat cccttgtttg ataagagaca aaagtgttgc 180
 ggccccggcg cgtcatgccc cagatatttc aaagacaatt ttatttgtagg ttgttgtaa 240
 atgacaacgt gtcgatgacc aacttcgtta tcacgacttc gccaaagtgtc taatgaataa 300
 gtaaaacgat tgcagt 316
 <210> 204
 <211> 73
 <212> PRT
 <213> Conus stercusmuscarum

<400> 204
 Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
 1 5 10 15
 Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro Ala
 20 25 30
 Asp Arg Met Gln Asn Asp Ile Ser Ser Glu Gln Tyr Pro Leu Phe Asp
 35 40 45
 Lys Arg Gln Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe
 50 55 60
 Lys Asp Asn Phe Ile Cys Gly Cys Cys
 65 70

<210> 205
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 and 11 is P
 ro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 205
 Xaa Lys Cys Cys Gly Xaa Gly Ala Ser Cys Xaa Arg Xaa Phe Lys Asp
 1 5 10 15
 Asn Phe Ile Cys Gly Cys Cys
 20

<210> 206
 <211> 331
 <212> DNA
 <213> Conus striatus

<400> 206
 cgacctttca agagggatcg atagcagttc gcgatgtcta aactgggggt attgttgacc 60
 atctgtctgc ttctgtttcc ccttactgct cttccgatgg atgaagatca acctgcagac 120
 caacttgaag atcgtatgca ggacgacatt tcacttgagc agtatccctc gtttgtagg 180
 agacaaaagt gttgcggcga aggtcgtca tgccccaaat atttcaaaaa caattttatt 240

tgtggttgtt gttaaataac aacgtgtcga tgaccaactt cggtatcacg actacgcaa 300

gtgtcttgtc taatgataat aaaatgattc c 331

<210> 207

<211> 73

<212> PRT

<213> Conus striatus

<400> 207

Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe Pro
1 5 10 15

Leu Thr Ala Leu Pro Met Asp Glu Asp Gln Pro Ala Asp Gln Leu Glu
20 25 30

Asp Arg Met Gln Asp Asp Ile Ser Ser Glu Gln Tyr Pro Ser Phe Val
35 40 45

Arg Arg Gln Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe
50 55 60

Lys Asn Asn Phe Ile Cys Gly Cys Cys
65 70

<210> 208

<211> 23

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 11 is Pro or Hyp; Xaa at residue 13 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 208

Xaa Lys Cys Cys Gly Xaa Gly Ser Ser Cys Xaa Lys Xaa Phe Lys Asn
1 5 10 15

Asn Phe Ile Cys Gly Cys Cys
20

<210> 209

<211> 256

<212> DNA

<213> Conus striatus

<400> 209

ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtttcccctt 60

actgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120

gacatttcat ctgacgagca tcccttgttt gataagagac aaaactgttg caatggggga 180

tgctccagca aatggtgcag agatcacgca cgttgttgcg gtcgatgata acgtgttgat 240

gaccaacttt ctcgag 256

<210> 210

<211> 75

<212> PRT

<213> Conus striatus

<400> 210

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Asp Glu His Pro
35 40 45

Leu Phe Asp Lys Arg Gln Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys
50 55 60

Trp Cys Arg Asp His Ala Arg Cys Cys Gly Arg
65 70 75

<210> 211

<211> 20

<212> PRT

<213> Conus striatus

<220>

<221> PEPTIDE

<222> (1)..(20)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 12 is Trp or bromo-Tr

<400> 211

Xaa Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Xaa Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 212

<211> 235

<212> DNA

<213> Conus tessulatus

<400> 212

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actgctgttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg taggcaggac 120

attgcaactg acgatcatcc tttgtttgat cccgtcaaac ggtgctgcca caaatgctat 180

atgggatgca tcccttggtg catttagtaa cgtgttgatg accaactttc tcgag 235

<210> 213

<211> 68

<212> PRT

<213> Conus tessulatus

<400> 213

Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Met Cys Leu Leu
1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
20 25 30

Arg Pro Ala Glu Arg Arg Gln Asp Ile Ala Thr Asp Asp His Pro Leu
35 40 45

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Phe Asp Pro Val Lys Arg Cys Cys His Lys Cys Tyr Met Gly Cys Ile
 50 55 60

Pro Cys Cys Ile
 65

<210> 214
 <211> 14
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 214
 Cys Cys His Lys Cys Xaa Met Gly Cys Ile Xaa Cys Cys Ile
 1 5 10

<210> 215
 <211> 238
 <212> DNA
 <213> Conus tessulatus

<400> 215
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtgtgcttct gtttcccctt 60
 actgctgttc cgctggatgg agatcaacct gcagaccaac ctgcagagcg tacgcagaac 120
 gagcagcatc ccttgtatga tcagaaaaga aagtgttgcc ggccgcatg cgccatgagc 180
 tgcggcatgg ctaggtgttg ctattaatga taacgtgttg atgaccaact ttctcgag 238

<210> 216
 <211> 68
 <212> PRT
 <213> Conus tessulatus

<400> 216
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Val Leu
 1 5 10 15

Leu Phe Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30

Gln Pro Ala Glu Arg Thr Gln Asn Glu Gln His Pro Leu Tyr Asp Gln
 35 40 45

Lys Arg Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala
 50 55 60

Arg Cys Cys Tyr
 65

<210> 217
 <211> 18
 <212> PRT
 <213> Conus tessulatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 5 and 6 is Pro or Hyp; Xaa at residue 18 is Tyr, 1

25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 217

Lys Cys Cys Arg Xaa Xaa Cys Ala Met Ser Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Xaa

<210> 218

<211> 564

<212> DNA

<213> Conus textile

<400> 218

gagtcaaccc actgtcacgc caagagcgga cgccacagct aaggcaagaa ggatcgatag 60
cagttcatga tgtctaaact gggagccttg ttgaccatct gtctacttct gttttccctt 120
actgctgttc cgctggatgg agatcaacat gcagaccaac ctgcacagcg tctgcaggac 180
cgcatcccaa ctgaagatca tcccttattt gatcccaaca aacggtgttg cccgccggtg 240
gcatgcaaca tgggatgcaa gccttggttg ggatgaccag ctttgttatc gcggtctcat 300
gaagtgtcta atgaataagt aaaacgattg cagtttcggt cagatttgct gttgtatttt 360
ggtctaaaga ttaatgacca aactgttctt ttgatccgga ttttcacgta tttctcgatt 420
cctattcaac actagataag ttaatcacga cagatctgat tttccatcaa tgccttgctt 480
tttggctgt catataaatc ttgtttatat ttaatttctc gtcactttca acacgcacac 540
acacacacac acacacgcgc gcgc 564

<210> 219

<211> 69

<212> PRT

<213> Conus textile

<400> 219

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
20 25 30

Ala Gln Arg Leu Gln Asp Arg Ile Pro Thr Glu Asp His Pro Leu Phe
35 40 45

Asp Pro Asn Lys Arg Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys
50 55 60

Lys Pro Cys Cys Gly
65

<210> 220

<211> 16

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 3, 4 and 13 is Pro or Hyp

<222> (1)..(12)

<223> Xaa at residue 10 is Pro or Hyp

<400> 223

Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 224

<211> 456

<212> DNA

<213> Conus textile

<400> 224

ggaacagtcac accccacagc cacgccaaga gcagacagcc acagctacgt gaagaagggt 60
ggagagaggt tcatgatgtt gaaaatggga gtggtgctat tcatctttct ggtactgttt 120
cccctggcaa cgctccagct ggatgcagat caacctgtag aacgatatgc ggagaacaaa 180
cagctcctca acccagatga aaggagggaa atcctattgc ctgctctgag gaagttctgc 240
tgtgattcga attggtgccca catttcggat tgtgagtgtt gctacggtta gcgccgaaca 300
tccatggcac tgtgctgggc ggtttcatcc caacaacgac agcgtttggt gatttcatgt 360
atcattgcgc ccacgtctct tgtctaagaa tgacgaacat gattgcactc tggttcagat 420
ttcgtgttct tttctgacaa taaatgacaa acctcc 456

<210> 225

<211> 70

<212> PRT

<213> Conus textile

<400> 225

Met Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe
1 5 10 15

Pro Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr
20 25 30

Ala Glu Asn Lys Gln Leu Leu Asn Pro Asp Glu Arg Arg Glu Ile Leu
35 40 45

Leu Pro Ala Leu Arg Lys Phe Cys Cys Asp Ser Asn Trp Cys His Asp
50 55 60

Cys Glu Cys Cys Tyr Gly
65 70

<210> 226

<211> 17

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Xaa at residue 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 is Trp or bromo-Trp; Xaa at residue 17 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 226

Phe Cys Cys Asp Ser Asn Xaa Cys His Ile Ser Asp Cys Xaa Cys Cys
1 5 10 15

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<210> 227
<211> 456
<212> DNA
<213> Conus textile
```

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<220>
<221> misc_feature
<222> (1)..(456)
<223> n may be any nucleotide
```

[illegible]

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<210> 228
<211> 70
<212> PRT
<213> Conus textile
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<400> 228
Met Leu Lys Met Gly Val Val Leu Phe Ile Phe Leu Val Leu Phe Pro
1      5      10     15
Leu Ala Thr Leu Gln Leu Asp Ala Asp Gln Pro Val Glu Arg Tyr Ala
20     25     30
Glu Asn Lys Gln Leu Leu Ser Pro Asp Glu Arg Arg Glu Ile Ile Leu
35     40     45
His Ala Leu Gly Thr Arg Cys Cys Ser Trp Asp Val Cys Asp His Pro
50     55     60
Ser Cys Thr Cys Cys Gly
65     70

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<210> 229
<211> 15
<212> PRT
<213> Conus textile
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<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 10 is Pro or Hyp; Xaa at residue 4 is Trp or bromo
      -Tr
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<400> 229
Cys Cys Ser Xaa Asp Val Cys Asp His Xaa Ser Cys Thr Cys Cys
1          5          10          15
```

<210> 230
 <211> 235
 <212> DNA
 <213> Conus textile

<400> 230
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccott 60
 actgtctcttc cgctggatgg agatcaaccc gcagaccaag ctgcagagcg tatgcaggcc 120
 gagcagcatc ccttgtttga tcagaaaaga cgggtgtgca agtttccatg ccccgatagt 180
 tgcagatatt tgtgttgcg gtgatgataa cgtgttgatg accaactttc tcgag 235

<210> 231
 <211> 67
 <212> PRT
 <213> Conus textile

<400> 231
 Gly Ser Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu
 1 5 10 15
 Leu Phe Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp
 20 25 30
 Gln Ala Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln
 35 40 45
 Lys Arg Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Arg Tyr Leu
 50 55 60
 Cys Cys Gly
 65

<210> 232
 <211> 16
 <212> PRT
 <213> Conus textile

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 8 is Pro or Hyp; Xaa at residue 13 is Tyr, 1
 25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 232
 Arg Cys Cys Lys Phe Xaa Cys Xaa Asp Ser Cys Arg Xaa Leu Cys Cys
 1 5 10 15

<210> 233
 <211> 321
 <212> DNA
 <213> Conus tulipa

<400> 233
 cgacctcaag agggatcgat agcagttcat gtctaaactg _yagtcttgt tgacaatctg 60
 tctgcttctg tttcccctta ctgotctgcc gatggatgga gatgaacctg cagaccgacc 120
 tgcagagcgt atgcaggaca acatttcatc tgagcagcat cccttgtttg aggagagaca 180
 cggatgttgc aaggggcccg aaggatgctc ctccagagaa tgcagacccc aacattgttg 240

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<210> 234
<211> 74
<212> PRT
<213> Conus tulipa
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Cys Arg Pro Gln His Cys Cys Gly Arg Arg
65 70

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<210> 235
<211> 21
<212> PRT
<213> Conus tulipa
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<220>
<221> PEPTIDE
<222> (1)..(21)
<223> Xaa at residue 8 and 14 is Glu or gamma-carboxy Glu; Xaa at residue 7 and 17 is Pro or Hy
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Xaa Gln His Cys Cys
20

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<210> 236
<211> 287
<212> DNA
<213> Conus figulinus
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<400> 236
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct    60
gcttctgatt ccccttactg ctcttttcgt ggatggagat caacctgcag accgacctgc   120
agagcgtatg caggatggaa ttcatctga acagcatccc atgtttgatc ccgtcagacg    180
gtgttgcccg tggccatgca acataggatg cgtaccttgt tgttgatgac cagttttgtt   240
atcgcgcct catcaaattg ctaatgaata agtaaaacga ttgcagt                287

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<210> 237
<211> 67
<212> PRT
<213> Conus figulinus
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<400> 237


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<210> 241
<211> 14
<212> PRT
<213> Conus figulinus
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<220>
<221> PEPTIDE
<222> (1)..(14)
<223> Xaa at residue 11 and 14 is Pro or Hyp
```

<400> 241
Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Xaa Cys Cys Xaa
1 5 10

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<210> 242
<211> 286
<212> DNA
<213> Conus figulinus
```

[illegible]

<210>	243
<211>	64
<212>	PRT
<213>	Conus figulinus

<400> 243
Met Met Ser Lys Leu Arg Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asn Glu Asp Gln Pro Ala Glu Arg Met
20 25 30

Gln Asp Asp Asn Ser Ser Glu Gln His Pro Leu Tyr Asp His Lys Arg
35 40 45

Lys Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
50 55 60

<210>	244
<211>	15
<212>	PRT
<213>	Conus figulinus

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<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 7 is Pro c_ Hyp; Xaa at residue 4 is Trp or
      bromo-Tr
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<400> 244
Cys Cys Arg Xaa Xaa Cys Xaa Ala Arg Cys Gly Ser Cys Cys Leu
1          5          10          15
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<210> 245

<211> 301
 <212> DNA
 <213> Conus figulinus

<400> 245
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caagctgcag accgacctgc 120
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180
 ttgcgagttg tcaagctgcc ttggatgcgt cccttggtgc acatcttaat aacgtgtgga 240
 tgaccaactg tgttatcacg gccacgtcaa gtgtctaata aataagtaaa atgattgcag 300
 t 301

<210> 246
 <211> 68
 <212> PRT
 <213> Conus figulinus

<400> 246
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Ala Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro
 50 55 60
 Cys Cys Thr Ser
 65

<210> 247
 <211> 16
 <212> PRT
 <213> Conus figulinus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 3 and 12 is Pro or Hyp

<400> 247
 Cys Cys Xaa Leu Ser Arg Cys Leu Gly Cys Val Xaa Cys Cys Thr Ser
 1 5 10 15

<210> 248
 <211> 301
 <212> DNA
 <213> Conus figulinus

<400> 248
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccttatgtct 60
 gcttctgttt cccctgactg ctcttccgct ggatgaagat caacctgcag accgacctgc 120
 agagcgtatg cagggcatgt catctgaaca gcatcccttc tttgatcccg tcaaacgggtg 180
 ttgcgagttg tcaaaatgcc atggatgcgt cccttggtgc ataccttaat aacgtgcgga 240

tgaccaactg tgttatcacg gccacgtcaa gtgtctaatag aataagtaaa atgattgcag 300
t 301

<210> 249
<211> 68
<212> PRT
<213> Conus figulinus

<400> 249
Met Met Ser Lys Leu Gly Val Leu Leu Thr Leu Cys Leu Leu Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
20 25 30
Ala Glu Arg Met Gln Gly Met Ser Ser Glu Gln His Pro Phe Phe Asp
35 40 45
Pro Val Lys Arg Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro
50 55 60
Cys Cys Ile Pro
65

<210> 250
<211> 16
<212> PRT
<213> Conus figulinus

<220>
<221> PEPTIDE
<222> (1)..(16)
<223> Xaa at residue 3 is Glu or gamma-carboxy Glu; Xaa at residue 12 and 16 is Pro or Hy

<400> 250
Cys Cys Xaa Leu Ser Lys Cys His Gly Cys Val Xaa Cys Cys Ile Xaa
1 5 10 15

<210> 251
<211> 298
<212> DNA
<213> Conus quercinus

<400> 251
caagagggat cgatagcagt tcatgatgtc taaactcgga gtcttgttga ccatctgtct 60
ggttctgttt ccccttacag ctcttcagct ggatggagat caacctgcag accgacctgc 120
agagcgtacg caggacattt catctgaaca gtatcgaaaag tttgatcaga gacagaggtg 180
ttgccggtgg ccatgccccg gtagttgcag atgctgccgt tatcgttaac gtgttggtga 240
ccagctttgt tatcaccgacc acgccaagtg tctaacgaat aagtaaaatg attgcagt 298

<210> 252
<211> 68
<212> PRT
<213> Conus quercinus

<400> 252
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Val Leu Phe
1 5 10 15
Pro Leu Thr Ala Leu Gln Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro

30

Leu Tyr Asp Pro Lys Arg Arg Cys Cys Arg Tyr Pro Cys Pro Asp Ser
50 55 60

<220>

Glu Glu Arg His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg
50 55 60

<211> 23
 <212> PRT
 <213> Conus aurisiacus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 1 is Gln or pyro-Glu

<400> 266
 Xaa Lys Cys Cys Thr Gly Arg Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
 20

<210> 267
 <211> 239
 <212> DNA
 <213> Conus betulinus

<400> 267
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccctt 60
 actgctgttc cgttggatgg agatcaacct gcagaccaac ctgcagagcg tatgcagaac 120
 gagcagcatc cctcgtttga tcagaaaaga aggtgctgcc ggtggccatg cccaggtata 180
 tgcggcatgg ctaggtgttg cttcgtcatg ataacgtgtt gatgaccaac tttctcgag 239

<210> 268
 <211> 71
 <212> PRT
 <213> Conus betulinus

<400> 268
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Ser Phe Asp Gln Lys Arg
 35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
 50 55 60

Cys Phe Val Met Ile Thr Cys
 65 70

<210> 269
 <211> 23
 <212> PRT
 <213> Conus betulinus

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or
 bromo-Tr

<400> 269
 Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

[illegible]

<210> 277
 <211> 75
 <212> PRT
 <213> Conus parius

<400> 277
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Leu
 20 25 30
 Val Glu Arg Met Gln Asp Asn Ile Ser Ser Glu Gln His Pro Phe Phe
 35 40 45
 Glu Lys Arg Arg Gly Cys Cys Thr Pro Pro Arg Lys Cys Lys Asp Arg
 50 55 60
 Ala Cys Lys Pro Ala Arg Cys Cys Gly Pro Gly
 65 70 75

<210> 278
 <211> 23
 <212> PRT
 <213> Conus parius

<220>
 <221> PEPTIDE
 <222> (1)..(23)
 <223> Xaa at residue 6, 7, 17 and 23 is Pro or Hyp

<400> 278
 Arg Gly Cys Cys Thr Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
 1 5 10 15
 Xaa Ala Arg Cys Cys Gly Xaa
 20

<210> 279
 <211> 241
 <212> DNA
 <213> Conus coronatus

<400> 279
 ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60
 actgcccttc cgctggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgctgcga ttggccatgc 180
 atcccaggat gcaccccttg ttgcttgcct tgataacgtg ttgatgacca actttctcga 240
 g 241

<210> 280
 <211> 68
 <212> PRT
 <213> Conus coronatus

<400> 280
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30

<210>	284
<211>	14
<212>	PRT

<220>

<222> (1) .. (14)

<400> 284

<210> 285

<211> 14

<212> PRT

<213> Conus betulinus

 $\langle 220 \rangle$

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (14)$

<400> 285

<210> 286

<211> 14

<212> PRT

<213> Conus betulinus

 $\langle 220 \rangle$

<221> PEPTIDE

<222> (1) .. (14)

<400> 286

<210> 287

<211> 235

<212> DNA

<213> Conus pennaceus

<400> 287

actgctcttc cgctggatgg agatcaacct gcataccaag ctgcagagcg tatgcaggcc 120

gagcatcatc ccttgtttga tcagaaaaga cggtgctgca agtttccatg ccccgatagt 180

tgcaaatatt tgtgttgctgg gtgatgataa catgttgatg accaactttc ttgag 235

<210> 288

<211> 65

<212> PRT

<213> Conus pennaceus

<400> 288

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Cys Cys Phe
65

<210> 292
 <211> 14
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(14)
 <223> Xaa at residue 11 is Pro or Hyp; Xaa at residue 6 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 292
 Cys Cys Val Ser Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
 1 5 10

<210> 293
 <211> 244
 <212> DNA
 <213> Conus pulicarius

<400> 293
 ggatccatga tgtctaaact gggagtcttg ttgaccgtct gtctgcttct gtgtccctt 60
 actgctcttc cactggatga agatcaactt gcagaccgac ctgcagagcg tatgcaggat 120
 gacacttcag ctgcacagat tttcgggttt gatcccgctca aacggtgctg caaattgcta 180
 tgctactcgg gatgcactcc ttgttgccat atttgataac gtgttgatga ccaactttct 240
 cgag 244

<210> 294
 <211> 67
 <212> PRT
 <213> Conus pulicarius

<400> 294
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Leu Pro Leu Asp Glu Asp Gln Leu Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Asp Thr Ser Ala Ala Gln Ile Phe Gly Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys
 50 55 60
 Cys His Ile
 65

<210> 295
 <211> 16
 <212> PRT
 <213> Conus pulicarius

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 295
 Cys Cys Lys Leu Leu Cys Xaa Ser Gly Cys Thr Xaa Cys Cys His Ile

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<210> 297
<211> 75
<212> PRT
<213> Conus rattus
```

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<210> 298
<211> 23
<212> PRT
<213> Conus rattus
```

<400> 298
Arg Gly Cys Cys Ala Xaa Xaa Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

```
<210> 299
<211> 262
<212> DNA
<213> Conus stercusmuscarum
```

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<400> 299
ggatccatga tgtctaaact gggagtcttg ttgacaatct gtctgcttct gtttcccctt      60
attgctcttc cgctggatgg agatcaacct gcagaccgac ctgcagagcg tatgcaggac      120

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<210>	303
<211>	67
<212>	PRT

50

55

60

Cys Cys Phe
65

<210> 307
<211> 15
<212> PRT
<213> Conus ebraceus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa at residue 5 and 12 is Pro or Hyp; Xaa at residue 7 is Tyr, 1
25I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 307
Cys Cys Ala Gln Xaa Cys Xaa Met Gly Cys Ile Xaa Cys Cys Phe
1 5 10 15

<210> 308
<211> 238
<212> DNA
<213> Conus flavidus

<400> 308
ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttcccctt 60
actgctgttc cgttggatgg agatcaacct gcagaccagc ctgcagagcg tatgcagaac 120
gagcagcatc ccttgtttga tcagaaaaga aggtgctgcc ggtggccatg ccccagtata 180
tgcgccatgg ctaggtgttg ctggtcatga taacgtgttg atgaccaact ttctcgag 238

<210> 309
<211> 67
<212> PRT
<213> Conus flavidus

<400> 309
Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Pro
20 25 30

Ala Glu Arg Met Gln Asn Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
50 55 60

Cys Ser Ser
65

<210> 310
<211> 19
<212> PRT
<213> Conus flavidus

<220>
<221> PEPTIDE
<222> (1)..(19)
<223> Xaa at residue 6 and 8 is Pro or Hyp; Xaa at residue 5 is Trp or

bromo-Tr

<400> 310

Arg Cys Cys Arg Xaa Xaa Cys Xaa Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Ser Ser

<210> 311

<211> 245

<212> DNA

<213> Conus miliaris

<220>

<221> misc_feature

<222> (1)..(245)

<223> n may be any nucleotide

<400> 311

ggatccatga tgtctaaact gggagtcttg ttgaccatct gtctgcttct gtttccaatt 60
 actgcccttc cactggatga agatcaacct gcagaccgac ctgcagagcg tatgcaggac 120
 attgcaactg aacagcatcc cttgtttgat cccgtcaaac ggtgttgcca ttggccatgc 180
 agcgcaggat gctacccttg ttgcttcctt taataacgtg ttgatgacca actnangnaa 240
 aaaaaa 245

<210> 312

<211> 68

<212> PRT

<213> Conus miliaris

<400> 312

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15

Pro Ile Thr Ala Leu Pro Leu Asp Glu Asp Gln Pro Ala Asp Arg Pro
 20 25 30

Ala Glu Arg Met Gln Asp Ile Ala Thr Glu Gln His Pro Leu Phe Asp
 35 40 45

Pro Val Lys Arg Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro
 50 55 60

Cys Cys Phe Pro
 65

<210> 313

<211> 16

<212> PRT

<213> Conus miliaris

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 5, 12 and 16 is Pro or Hyp; Xaa at residue 4 is Trp or bromo-Trp; Xaa at residue 11 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 313

Cys Cys Asp Xaa Xaa Cys Ser Ala Gly Cys Xaa Xaa Cys Cys Phe Xaa
 1 5 10 15

```
<220>
<221> misc_feature
<222> (1)..(230)
<223> n may be any nucleotide
<400> 314
```

```
<210> 315
<211> 66
<212> PRT
<213> Conus miliaris
```

```
<210> 316
<211> 16
<212> PRT
<213> Conus miliaris
```

<400> 316
Gly Cys Cys Xaa Xaa Met Cys Thr Xaa Cys Phe Xaa Cys Cys Phe Arg
1 5 10 15

```
<400> 317
caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct    60
gcttctgttt ccccttactg ctcttcgcgt ggatggagat caacctgcag accaagctgc    120
```

agagcgtatg caggccgagc agcatccctt gtttgatcag aaaagacggt gttgcaggtt 180

tccatgcccc gatacttgca gacatttgtg ttgcgggtga tgataacgtg ctgatgaccc 240

actttgtcat cacggctacg tcaagtgtct aatgaataa; taaaatgatt gcagt 295

<210> 318

<211> 65

<212> PRT

<213> Conus ammiralis

<400> 318

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Thr Ala Leu Pro Leu Asp Gly Asp Gln Pro Ala Asp Gln Ala
20 25 30

Ala Glu Arg Met Gln Ala Glu Gln His Pro Leu Phe Asp Gln Lys Arg
35 40 45

Arg Cys Cys Arg Phe Pro Cys Pro Asp Thr Cys Arg His Leu Cys Cys
50 55 60

Gly
65

<210> 319

<211> 16

<212> PRT

<213> Conus ammiralis

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa at residue 6 and 8 is Pro or Hyp

<400> 319

Arg Cys Cys Arg Phe Xaa Cys Xaa Asp Thr Cys Arg His Leu Cys Cys
1 5 10 15

<210> 320

<211> 267

<212> DNA

<213> Conus ammiralis

<400> 320

caagagggat cgatagcagt tcatgatgtt taaactggga gtcttgctga ccatctgtct 60

acttctgttt tcccttaatg ctgttccgct ggatggagat caacctgcag accaacctgc 120

agagcgtctg ctggacgaca tttcatctga aaataatccc ttttatgatc ccgccaaacg 180

gtgttgcatg acttgcttcg gttgcacacc ttgttggtga tgaccagcct catcaagtgt 240

ctaacgaata agtaaaacga ttgcagt 267

<210> 321

<211> 66

<212> PRT

<213> Conus ammiralis

<400> 321

Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

$\langle 210 \rangle$	325
$\langle 211 \rangle$	18

<212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 325
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
 1 5 10 15

Phe Ser

<210> 326
 <211> 284
 <212> DNA
 <213> Conus ammiralis

<400> 326
 caagagggat cgatagcagt tcatgatgtt taaactcgga gtcttgctga ccatctgtct 60
 acttctgttt tocctaattg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg caggaccgcc ttccaactga aaatcatccc ttatatgatc ccgtcaaacg 180
 gtgttgccagg ttgttatgcc tcagttgcaa cccttgttgt ggatgaccag ctttgttatc 240
 acggcctcat caagtgtcta atgaataagt aaaacgattg cagt 284

<210> 327
 <211> 67
 <212> PRT
 <213> Conus ammiralis

<400> 327
 Met Met Phe Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Arg Leu Leu Cys Leu Ser Cys Asn Pro
 50 55 60

Cys Cys Gly
 65

<210> 328
 <211> 13
 <212> PRT
 <213> Conus ammiralis

<220>
 <221> PEPTIDE
 <222> (1)..(13)
 <223> Xaa at residue 11 is Pro or Hyp

<400> 328

<400> 332
caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccattctgtct 60

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<210> 333
<211> 63
<212> PRT
<213> Conus spurius
```

Lys Arg Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys Gly
50 55 60

```
<210> 334
<211> 12
<212> PRT
<213> Conus spurius
```

```
<220>
<221>  PEPTIDE
<222>  (1)..(12)
<223>  Xaa at residue 7 is Glu or gamma-carboxy Glu; Xaa at residue 3 and
      d 10 is Pro or Hy
```

<400> 334
Cys Cys Xaa Arg Cys Ser Xaa Cys Asn Xaa Cys Cys
1 5 10

```
<210> 335
<211> 293
<212> DNA
<213> Conus omaria
```

[illegible]

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<210> 336
<211> 70
<212> PRT
<213> Conus omaria
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<400> 336
Met Met Ser Lys Leu Gly Val Ser Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Cys Thr Pro Cys Asp Cys
65 70

<210> 340
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue is 14 Pro or Hyp; Xaa at residue 6 is Trp or bromo-
 -Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr,
 O-sulpho-Tyr or O-phospho-Ty

<400> 340
 Cys Cys Lys Xaa Gly Xaa Thr Cys Leu Leu Gly Cys Thr Xaa Cys Asp
 1 5 10 15

Cys

<210> 341
 <211> 290
 <212> DNA
 <213> Conus omaria

<400> 341
 caagagggat cgatagcagt tcatgatgtc tatactggga gtcttggtga tcatctgtct 60
 acttctgtgt ccccttactg ctgttctgga ggatggagat caacctgcag accgacctgc 120
 agagcgtatg caggacggca tttcatctga acatcatccc tttttggatc ccgtaaacg 180
 gtgttgccat ctattggcat gccgctttgg atgctgcct tgttggtggt gaccagcttt 240
 gttatcgcg g cctcatcaag tgtctaataa ataagtaaaa cgattgcagt 290

<210> 342
 <211> 69
 <212> PRT
 <213> Conus omaria

<400> 342
 Met Met Ser Ile Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Val Leu Glu Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Asp Gly Ile Ser Ser Glu His His Pro Phe Leu
 35 40 45
 Asp Pro Val Lys Arg Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys
 50 55 60

Ser Pro Cys Cys Trp
 65

<210> 343
 <211> 16
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 13 is Pro or Hyp; Xaa at residue 16 is Trp or bromo-
 o-Tr

<400> 343
 Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Xaa Cys Cys Xaa
 1 5 10 15

<210> 344
 <211> 293
 <212> DNA
 <213> Conus omaria

<400> 344
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60
 acttctttgt ccccttactg ctgttccgca ggatggagat caacctgcag accgacctgc 120
 agagcgtatg cagggcggca tttcatctga acatcatccc ttttttgatc ccgtcaaacg 180
 gtgttgcaagg tacgggtgga catgctggct aggatgcact ccctgtgggtt gttgaccagc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 345
 <211> 70
 <212> PRT
 <213> Conus omaria

<400> 345
 Met Met Ser Lys Leu Gly Val Leu Leu Ile Ile Cys Leu Leu Leu Cys
 1 5 10 15
 Pro Leu Thr Ala Val Pro Gln Asp Gly Asp Gln Pro Ala Asp Arg Pro
 20 25 30
 Ala Glu Arg Met Gln Gly Gly Ile Ser Ser Glu His His Pro Phe Phe
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly
 50 55 60
 Cys Thr Pro Cys Gly Cys
 65 70

<210> 346
 <211> 17
 <212> PRT
 <213> Conus omaria

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 14 is Pro or Hyp; Xaa at residue 6 and 9 is Trp or
 bromo-Trp; Xaa at residue 4 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-
 iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 346
 Cys Cys Arg Xaa Gly Xaa Thr Cys Xaa Leu Gly Cys Thr Xaa Cys Gly
 1 5 10 15

Cys

<210> 347
 <211> 293
 <212> DNA
 <213> Conus episcopatus

PEPTIDE

<400> 347
 caagaaggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcatg gaggacgaat gcaacagttc atgctggcct tgttggtggg ggtgatcagc 240
 tttgttatcg cggcctgac aagtgtataa tgaataagta aaacgattgc agt 293

<210> 348
 <211> 70
 <212> PRT
 <213> Conus episcopatus

<400> 348
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys
 50 55 60
 Trp Pro Cys Cys Trp Gly
 65 70

<210> 349
 <211> 16
 <212> PRT
 <213> Conus episcopatus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 349
 Cys Cys Asp Xaa Asp Xaa Cys Asn Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 350
 <211> 293
 <212> DNA
 <213> Conus episcopatus

<400> 350
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttattg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttatgc ctgtcaaacg 180
 gtgttgcatg gaggacgaat gcagcagttc atgctggcct tgttggtggg gatgagcagc 240
 tttgttatcg cggcctcatc aagtgtctaa tgaataagta aaacgattgc agt 293

<210> 351
 <211> 70

<212> PRT
 <213> Conus episcopatus

<400> 351
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Ile Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Met Pro Val Lys Arg Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys
 50 55 60
 Trp Pro Cys Cys Trp Gly
 65 70

<210> 352
 <211> 16
 <212> PRT
 <213> Conus episcopatus
 <220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa at residue 4 and 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 and 16 is Trp or bromo-Trp

<400> 352
 Cys Cys Asp Xaa Asp Xaa Cys Ser Ser Ser Cys Xaa Xaa Cys Cys Xaa
 1 5 10 15

<210> 353
 <211> 290
 <212> DNA
 <213> Conus episcopatus

<400> 353
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccattctgtct 60
 atttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180
 gtgttgcccc gggcgcat gtgccatggg atgcaagcct tgttggtgat gagcagcttt 240
 gttatcgtgg cctcatcaag tgtctaata gaataagtaaaa cgattgcagt 290

<210> 354
 <211> 69
 <212> PRT
 <213> Conus episcopatus

<400> 354
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45

```
<220>
<221>  PEPTIDE
<222>  (1)..(16)
<223>  Xaa at residue 5 and 6 is Pro or Hyp
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<400> 358
 Gly Cys Cys Ser Xaa Xaa Cys His Ser Ile Cys Ala Ala Phe Cys Cys
 1 5 10 15

<210> 359
 <211> 290
 <212> DNA
 <213> Conus aulicus

<400> 359
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
 acttctgttt tcccttactg ctgttccgct tgatggagat caacatgcag accaacctgc 120
 agagcgtctg cagggcgaca ttttatctga aaagcatccc ttatttaatc ccgtcaaacg 180
 gtgttgccga cgggtggcat gtgccatggg atgcaagcct tgttggtgat gacgagcttt 240
 gttatcgtgg cctcatcaag tgtctaataa ataagtaaaa tgattgcagt 290

<210> 360
 <211> 69
 <212> PRT
 <213> Conus aulicus

<400> 360
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Gly Asp Ile Leu Ser Glu Lys His Pro Leu Phe
 35 40 45
 Asn Pro Val Lys Arg Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys
 50 55 60
 Lys Pro Cys Cys Gly
 65

<210> 361
 <211> 15
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (1)..(15)
 <223> Xaa at residue 4 and 13 is Pro or Hyp

<400> 361
 Cys Cys Arg Xaa Val Ala Cys Ala Met Gly Cys Lys Xaa Cys Cys
 1 5 10 15

<210> 362
 <211> 290
 <212> DNA
 <213> Conus aulicus

<400> 362
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga tcatctgtct 60
 acttctgtct ccccttactg ctgttccgct ggatggagat caacctgcag accgacctgc 120

```
<210> 363
<211> 69
<212> PRT
<213> Conus aulicus
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Pro Leu Thr Ala Val Pro Leu Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Asp Ala Ile Arg Gln Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys
50 55 60

```
<210> 364
<211> 16
<212> PRT
<213> Conus aulicus
```

<400> 364
Xaa Cys Cys Xaa Ala Val Ala Cys Ala Met Gly Cys Xaa Xaa Cys Cys
1 5 10 15

```

<400> 365
caagaaggat cgatagcagt tcatgatgtc taaactggga gccttgttga ccatctgtct 60
acttctgttt tcccttactg ctgttccgct ggatggagat caacatgcag accaacatgc 120
agagcgtctg catgaccgcc ttccaactga aaatcatccc ttatatgata ccggtcaaacg 180
gtgttgcgat gattcggaat gcgactattc ttgctggcct tgctgtattt ttggataacc 240
tttgttatcg cggcctcatc aagtgtcaaa tgaataagta aaacgattgc agt 293

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<400> 366

Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln His
 20 25 30
 Ala Glu Arg Leu His Asp Arg Leu Pro Thr Glu Asn His Pro Leu Tyr
 35 40 45
 Asp Pro Val Lys Arg Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys
 50 55 60
 Trp Pro Cys Cys Ile Phe Gly
 65 70

<210> 367
 <211> 17
 <212> PRT
 <213> Conus aureus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa at residue 6 is Glu or gamma-carboxy Glu; Xaa at residue 13 is Pro or Hyp; Xaa at residue 12 is Trp or bromo-Trp; Xaa at residue 9 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 367
 Cys Cys Asp Asp Ser Xaa Cys Asp Xaa Ser Cys Xaa Xaa Cys Cys Ile
 1 5 10 15

Phe

<210> 368
 <211> 290
 <212> DNA
 <213> Conus aureus

<400> 368
 caagagggat cgatagcagt tcatgatgtc taaactggga gccttggtga ccattctgtct 60
 acttctgttt tccctaactg ctgttccgct ggatggagat caacatgcag accaacctgc 120
 agagcgtctg caggaccgca ttccaactga aaatcatccc ttatttgatc cgaacaaacg 180
 gtgttgcaat gattgggaat gcgacgattc atgctggcct tgctgttatg gataaccttt 240
 gttatcgcgg cctcatcaag tgtcaaatga ataagtaaaa cgattgcagt 290

<210> 369
 <211> 70
 <212> PRT
 <213> Conus aureus

<400> 369
 Met Met Ser Lys Leu Gly Ala Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Ser Leu Thr Ala Val Pro Leu Asp Gly Asp Gln His Ala Asp Gln Pro
 20 25 30
 Ala Glu Arg Leu Gln Asp Arg Ile Pro Thr Glu Asn His Pro Leu Phe
 35 40 45

<210>	373
<211>	22
<212>	PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 5 is Glu or gamma-carboxy Glu; Xaa at residue 8 and 10 is Pro or Hyp; Xaa at residue 12 is Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phospho-Ty

<400> 373

Met Cys Cys Gly Xaa Gly Ala Xaa Cys Xaa Ser Xaa Phe Arg Asn Ser
1 5 10 15

Gln Ile Cys His Cys Cys
20

<210> 374

<211> 315

<212> DNA

<213> Conus consors

<400> 374

taagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ccatctgtct 60
gcttctgttt ccccttattg ctcttccaat ggatggagat caacctgcag accgacctgc 120
agagcgtatg caggacgaca tttcatctca gcagcatccc ttgtttgata agagaggccg 180
ctgttgcgat gtgccgaacg catgctccgg cagatggtgc agagatcacg cacaatgttg 240
cggatgacga taacgtgttg atgaccaact ttgtgatcac ggctacatca agtgaataag 300
taaaacgatt gcagt 315

<210> 375

<211> 74

<212> PRT

<213> Conus consors

<400> 375

Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
1 5 10 15

Pro Leu Ile Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Arg Pro
20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Gln Gln His Pro Leu Phe
35 40 45

Asp Lys Arg Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg
50 55 60

Trp Cys Arg Asp His Ala Gln Cys Cys Gly
65 70

<210> 376

<211> 22

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(22)

<223> Xaa at residue 7 is Pro or Hyp; Xaa at residue 14 is Trp or bromo-Tr

<400> 376

Gly Arg Cys Cys Asp Val Xaa Asn Ala Cys Ser Gly Arg Xaa Cys Arg
 1 5 10 15

Asp His Ala Gln Cys Cys
 20

<210> 377

<211> 322

<212> DNA

<213> Conus consors

<400> 377

caagagggat cgatagcagt tcatgatgtc taaactggga gtcttggtga ctgtctgttt 60
 gcttctgttt ccccttactg ctcttccgat ggatggagat caacctgcag accaacctgc 120
 agagcgtatg caggacgaca tttcatctga gcagcatccc ttgtttgata agagacaaag 180
 gtgttgcaact gggaagaagg ggtcatgctc cggtaaagca tgcaaaagtc tcaaagtgtg 240
 ctctggacga taacgtgttg atgaccaact ttgttatcac ggctacgtca agtgtctagt 300
 gaataagtaa aacgattgca gt 322

<210> 378

<211> 76

<212> PRT

<213> Conus consors

<400> 378

Met Met Ser Lys Leu Gly Val Leu Leu Thr Val Cys Leu Leu Leu Phe
 1 5 10 15

Pro Leu Thr Ala Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Gln Pro
 20 25 30

Ala Glu Arg Met Gln Asp Asp Ile Ser Ser Glu Gln His Pro Leu Phe
 35 40 45

Asp Lys Arg Gln Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly
 50 55 60

Lys Ala Cys Lys Ser Leu Lys Cys Cys Ser Gly Arg
 65 70 75

<210> 379

<211> 23

<212> PRT

<213> Conus consors

<220>

<221> PEPTIDE

<222> (1)..(23)

<223> Xaa at residue 1 is Gln or pyro-Glu

<400> 379

Xaa Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Ser Leu Lys Cys Cys Ser
 20

<210> 380

<211> 284
 <212> DNA
 <213> Conus emaciatus

<400> 380
 caagagggat cgatagcagt tcatgatgtc taaactggga gtcttgctga ccatctgtct 60
 gcttctgttt ccccttactg ttcttccgat ggatggagat caacctgcag acctacctgc 120
 attgctgtcg cagttctttg cacctgaaca tagtccccgg ttgacccccg tcaaacggtg 180
 ctgctcgcgg gattgcagtg ttgcatccc ttgttgcccg tatggatcac cttgattatt .240
 gcggccacgt caagtgtcta atgaataagt aaaatgattg cagt 284

<210> 381
 <211> 70
 <212> PRT
 <213> Conus emaciatus

<400> 381
 Met Met Ser Lys Leu Gly Val Leu Leu Thr Ile Cys Leu Leu Leu Phe
 1 5 10 15
 Pro Leu Thr Val Leu Pro Met Asp Gly Asp Gln Pro Ala Asp Leu Pro
 20 25 30
 Ala Leu Arg Ala Gln Phe Phe Ala Pro Glu His Ser Pro Arg Phe Asp
 35 40 45
 Pro Val Lys Arg Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys
 50 55 60
 Cys Pro Tyr Gly Ser Pro
 65 70

<210> 382
 <211> 18
 <212> PRT
 <213> Conus emaciatus

<220>
 <221> PEPTIDE
 <222> (1)..(18)
 <223> Xaa at residue 11, 14 and 18 is Pro or Hyp; Xaa at residue 15 is
 Tyr, 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or O-phos
 pho-Ty

<400> 382
 Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Xaa Cys Cys Xaa Xaa Gly
 1 5 10 15

Ser Xaa

<210> 383
 <211> 13
 <212> PRT
 <213> Conus aurisiacus

<400> 383
 Cys Cys Lys Val Gln Cys Glu Ser Cys Thr Pro Cys Cys
 1 5 10

<210> 384
 <211> 15

$\langle 210 \rangle$	391
$\langle 211 \rangle$	14

Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Lys Pro Cys Cys Gly
1 5 10 15

<213> Conus marmoreus

<223> Xaa is Hyp

Ser Lys Gln Cys Cys His Leu Ala Ala Cys Arg Phe Gly Cys Thr Xaa
1 5 10 15

<213> Conus capitaneus

Ser Cys Cys Arg Asp Cys Gly Glu Asp Cys Val Gly Cys Cys Arg
1 5 10 15

<213> Conus coronatus

Cys Cys Asp Trp Pro Cys Ile Pro Gly Cys Thr Pro Cys Cys Leu Pro
1 5 10 15

<213> Conus dalli

Cys Cys Asp Asp Ser Glu Cys Asp Tyr Ser Cys Trp Pro Cys Cys Ile
1 5 10 15

<213> Conus dalli

Glx Gln Cys Cys Pro Pro Val Ala Cys Asn Met Gly Cys Glu Pro Cys
1 5 10 15

<213> Conus dalli

Cys Cys Asn Ala Gly Phe Cys Arg Phe Gly Cys Thr Pro Cys Cys Trp
1 5 10 15

<213> Conus distans

Glx Cys Cys Val His Pro Cys Pro Cys Thr Pro Cys Cys Arg
1 5 10

<213> Conus figulinus

Cys Cys Pro Trp Pro Cys Asn Ile Gly Cys Val Pro Cys Cys
1 5 10

<213> Conus figulinus

Cys Cys Ser Lys Asn Cys Ala Val Cys Ile Pro Cys Cys Pro
1 5 10

<213> Conus figulinus

Cys Cys Arg Trp Pro Cys Pro Ala Arg Cys Gly Ser Cys Cys Leu
1 5 10 15

<213> Conus figulinus

Cys Cys Glu Leu Ser Arg Cys Leu Gly Cys Val Pro Cys Cys Thr Ser
1 5 10 15

<213> Conus figulinus

Cys Cys Glu Leu Ser Lys Cys His Gly Cys Val Pro Cys Cys Ile Pro
1 5 10 15

<213> Conus generalis

<400> 410

Cys Cys His

<213> Conus lividus

Cys Cys His

<213> Conus marmoreus

<213> Conus marmoreus

Val

<213> Conus marmoreus

Cys Cys Trp

<213> Conus marmoreus

Cys

<213> Conus musicus

<400> 423

<400> 429

Cys Cys Ser Gln Asp Cys Leu Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 430
<211> 15
<212> PRT
<213> Conus quercinus

<220>
<221> PEPTIDE
<222> (1)..(15)
<223> Xaa is Hyp

<400> 430
Cys Cys Ser Arg His Cys Trp Val Cys Ile Xaa Cys Cys Pro Asn
1 5 10 15

<210> 431
<211> 16
<212> PRT
<213> Conus rattus

<400> 431
Glx Thr Cys Cys Ser Asn Cys Gly Glu Asp Cys Asp Gly Cys Cys Gln
1 5 10 15

<210> 432
<211> 20
<212> PRT
<213> Conus striatus

<400> 432
Glx Asn Cys Cys Asn Gly Gly Cys Ser Ser Lys Trp Cys Arg Asp His
1 5 10 15

Ala Arg Cys Cys
20

<210> 433
<211> 12
<212> PRT
<213> Conus textile

<220>
<221> PEPTIDE
<222> (1)..(12)
<223> Xaa is Hyp

<400> 433
Cys Cys Arg Thr Cys Phe Gly Cys Thr Xaa Cys Cys
1 5 10

<210> 434
<211> 14
<212> PRT
<213> Conus tessulatus

<400> 434
Cys Cys His Lys Cys Tyr Met Gly Cys Ile Pro Cys Cys Ile
1 5 10

<210> 435
<211> 18
<212> PRT
<213> Conus tessulatus

<400> 435

Lys Cys Cys Arg Pro Pro Cys Ala Met Ser Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Tyr

<210> 436

<211> 23

<212> PRT

<213> Conus betulinus

<400> 436

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
 20

<210> 437

<211> 23

<212> PRT

<213> Conus betulinus

<400> 437

Arg Cys Cys Arg Trp Pro Cys Pro Ser Arg Cys Gly Met Ala Arg Cys
 1 5 10 15

Cys Phe Val Met Ile Thr Cys
 20

<210> 438

<211> 15

<212> PRT

<213> Conus textile

<400> 438

Phe Cys Cys Asp Ser Asn Trp Cys His Asp Cys Glu Cys Cys Tyr
 1 5 10 15

<210> 439

<211> 16

<212> PRT

<213> Conus marmoreus

<400> 439

Cys Cys His Trp Asn Trp Cys Asp His Leu Cys Ser Cys Cys Gly Ser
 1 5 10 15

<210> 440

<211> 16

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is Hyp

<400> 440

Asp Cys Cys Xaa Leu Pro Ala Cys Pro Phe Gly Cys Asn Xaa Cys Cys
 1 5 10 15

<210> 441

<211> 16

<212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa is Hyp

<400> 441
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 442
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(16)
 <223> Xaa is Hyp

<400> 442
 Cys Cys Ala Xaa Ser Ala Cys Arg Leu Gly Cys Arg Xaa Cys Cys Arg
 1 5 10 15

<210> 443
 <211> 16
 <212> PRT
 <213> Conus marmoreus

<400> 443
 Cys Cys Ala Pro Ser Ala Cys Arg Leu Gly Cys Arg Pro Cys Cys Arg
 1 5 10 15

<210> 444
 <211> 17
 <212> PRT
 <213> Conus marmoreus

<220>
 <221> PEPTIDE
 <222> (1)..(17)
 <223> Xaa is Hyp

<400> 444
 Gly Cys Cys Gly Ser Phe Ala Cys Arg Phe Gly Cys Val Xaa Cys Cys
 1 5 10 15

Val

<210> 445
 <211> 15
 <212> PRT
 <213> Conus textile

<400> 445
 Cys Cys Ser Trp Asp Val Cys Asp His Pro Ser Cys Thr Cys Cys
 1 5 10 15

<210> 446
 <211> 16
 <212> PRT
 <213> Conus textile

<400> 446

Arg	Cys	Cys	Lys	Phe	Pro	Cys	Pro	Asp	Ser	Cys	Arg	Tyr	Leu	Cys	Cys
1				5					10					15	

<210> 447

<211> 17

<212> PRT

<213> Conus aureus

<400> 447

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe

<210> 448

<211> 16

<212> PRT

<213> Conus aureus

<400> 448

Cys	Cys	Asn	Asp	Trp	Glu	Cys	Asp	Asp	Ser	Cys	Trp	Pro	Cys	Cys	Tyr
1				5					10					15	

<210> 449

<211> 16

<212> PRT

<213> Conus ammiralis

<400> 449

Arg	Cys	Cys	Arg	Phe	Pro	Cys	Pro	Asp	Thr	Cys	Arg	His	Leu	Cys	Cys
1				5					10					15	

<210> 450

<211> 12

<212> PRT

<213> Conus ammiralis

<400> 450

Cys	Cys	Met	Thr	Cys	Phe	Gly	Cys	Thr	Pro	Cys	Cys
1				5					10		

<210> 451

<211> 18

<212> PRT

<213> Conus ammiralis

<400> 451

Cys	Cys	Asp	Asp	Ser	Glu	Cys	Asp	Tyr	Ser	Cys	Trp	Pro	Cys	Cys	Ile
1				5					10					15	

Phe Ser

<210> 452

<211> 13

<212> PRT

<213> Conus ammiralis

<400> 452

Cys	Cys	Arg	Leu	Leu	Cys	Leu	Ser	Cys	Asn	Pro	Cys	Cys
1				5					10			

<210> 453

<211> 16

<212> PRT

<213> Conus ammiralis

<400> 453

Cys Cys Asp Asp Ser Glu Cys Gly Tyr Ser Cys Trp Pro Cys Cys Tyr
1 5 10 15

<210> 454

<211> 16

<212> PRT

<213> Conus aulicus

<400> 454

Gly Cys Cys Ser Pro Pro Cys His Ser Ile Cys Ala Ala Phe Cys Cys
1 5 10 15

<210> 455

<211> 15

<212> PRT

<213> Conus aulicus

<400> 455

Cys Cys Arg Pro Val Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 456

<211> 16

<212> PRT

<213> Conus aulicus

<400> 456

Glx Cys Cys Pro Ala Val Ala Cys Ala Met Gly Cys Glu Pro Cys Cys
1 5 10 15

<210> 457

<211> 18

<212> PRT

<213> Conus emaciatus

<400> 457

Cys Cys Ser Arg Asp Cys Ser Val Cys Ile Pro Cys Cys Pro Tyr Gly
1 5 10 15

Ser Pro

<210> 458

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 458

Cys Cys Asp Glu Asp Glu Cys Asn Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 459

<211> 16

<212> PRT

<213> Conus episcopatus

<400> 459

Cys Cys Asp Glu Asp Glu Cys Ser Ser Ser Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 460

<211> 15

<212> PRT

<213> Conus episcopatus

<400> 460

Cys Cys Pro Ala Ala Ala Cys Ala Met Gly Cys Lys Pro Cys Cys
1 5 10 15

<210> 461

<211> 16

<212> PRT

<213> Conus omaria

<400> 461

Cys Cys Asp Glu Glu Glu Cys Ser Ser Ala Cys Trp Pro Cys Cys Trp
1 5 10 15

<210> 462

<211> 16

<212> PRT

<213> Conus omaria

<400> 462

Cys Cys His Leu Leu Ala Cys Arg Phe Gly Cys Ser Pro Cys Cys Trp
1 5 10 15

<210> 463

<211> 12

<212> PRT

<213> Conus spurius

<400> 463

Cys Cys Pro Arg Cys Ser Glu Cys Asn Pro Cys Cys
1 5 10

<210> 464

<211> 16

<212> PRT

<213> Conus pennaceus

<400> 464

Arg Cys Cys Lys Phe Pro Cys Pro Asp Ser Cys Lys Tyr Leu Cys Cys
1 5 10 15

<210> 465

<211> 19

<212> PRT

<213> Conus flavidus

<400> 465

Arg Cys Cys Arg Trp Pro Cys Pro Ser Ile Cys Gly Met Ala Arg Cys
1 5 10 15

Cys Ser Ser

<210> 466

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 466

Cys Cys Lys Leu Leu Cys Gly Cys Thr Pro Cys Cys His Ile
1 5 10

<210> 467

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 467

Cys Cys Glu Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 468

<211> 15

<212> PRT

<213> Conus ebraceus

<400> 468

Cys Cys Ala Gln Pro Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10 15

<210> 469

<211> 14

<212> PRT

<213> Conus pulicarius

<400> 469

Cys Cys Val Ser Cys Tyr Met Gly Cys Ile Pro Cys Cys Phe
1 5 10

<210> 470

<211> 16

<212> PRT

<213> Conus miliaris

<400> 470

Cys Cys Asp Trp Pro Cys Ser Ala Gly Cys Tyr Pro Cys Cys Phe Pro
1 5 10 15

<210> 471

<211> 16

<212> PRT

<213> Conus miliaris

<400> 471

Gly Cys Cys Pro Pro Met Cys Thr Pro Cys Phe Pro Cys Cys Phe Arg
1 5 10 15

<210> 472

<211> 23

<212> PRT

<213> Conus rattus

<400> 472

Arg Gly Cys Cys Ala Pro Pro Arg Lys Cys Lys Asp Arg Ala Cys Lys
1 5 10 15

Pro Ala Arg Cys Cys Gly Pro
20

<210> 473

<211> 22

<212> PRT

<213> Conus stercusmuscarum

<400> 473

Glx Arg Cys Cys Asn Gly Arg Arg Gly Cys Ser Ser Arg Trp Cys Arg
1 5 10 15

Asp His Ser Arg Cys Cys
20

<210> 474
 <211> 22
 <212> PRT
 <213> Conus consors

<400> 474
 Gly Arg Cys Cys Asp Val Pro Asn Ala Cys Ser Gly Arg Trp Cys Arg
 1 5 10 15
 Asp His Ala Gln Cys Cys
 20

<210> 475
 <211> 23
 <212> PRT
 <213> Conus consors

<400> 475
 Glx Arg Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15
 Lys Ser Leu Lys Cys Cys Ser
 20

<210> 476
 <211> 22
 <212> PRT
 <213> Conus aurisiacus

<400> 476
 Met Cys Cys Gly Glu Gly Arg Lys Cys Pro Ser Tyr Phe Arg Asn Ser
 1 5 10 15
 Gln Ile Cys His Cys Cys
 20

<210> 477
 <211> 19
 <212> PRT
 <213> Conus aurisiacus

<400> 477
 Cys Cys Arg Trp Pro Cys Pro Arg Gln Ile Asp Gly Glu Tyr Cys Gly
 1 5 10 15
 Cys Cys Leu

<210> 478
 <211> 22
 <212> PRT
 <213> Conus bullatus

<400> 478
 Arg Cys Cys Gly Glu Gly Leu Thr Cys Pro Arg Tyr Trp Lys Asn Ser
 1 5 10 15
 Gln Ile Cys Ala Cys Cys
 20

<210> 479
 <211> 21
 <212> PRT
 <213> Conus characteristicus

<400> 479

123 474 475 476 477 478 479

Asn Phe Ile Cys Gly Cys
20

<400> 485
Glx Lys Cys Cys Gly Pro Gly Gly Ser Cys Pro Val Tyr Phe Arg Asp
1 5 10 15
Asn Phe Ile Cys Gly Cys Cys
20

```

<400> 486
Glx Lys Cys Cys Gly Glu Gly Ser Ser Cys Pro Lys Tyr Phe Lys Asn
1          5          10          15
Asn Phe Ile Cys Gly Cys Cys
          20

```

```

<400> 487 ~
Glx Lys Cys Cys Ser Gly Gly Ser Cys Pro Leu Tyr Phe Arg Asp Arg
1          5          10          15
Leu Ile Cys Pro Cys Cys
          20

```

```
<400> 488
Glx Lys Cys Cys Gly Pro Gly Ala Ser Cys Pro Arg Tyr Phe Lys Asp
1      .      5      10      15
Asn Phe Ile Cys Gly Cys Cys
      20
```

Met Cys Cys Gly Glu Gly Ala Pro Cys Pro Ser Tyr Phe Arg Asn Ser
1 5 10 15
Gln Ile Cys His Cys Cys
20

```
<210> 490
<211> 23
<212> PRT
<213> Conus aurisiacus
```

<400> 490

Glx	Lys	Cys	Cys	Thr	Gly	Lys	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

<210> 491

<211> 23

<212> PRT

<213> Conus aurisiacus

<400> 491

Glx	Lys	Cys	Cys	Thr	Gly	Arg	Lys	Gly	Ser	Cys	Ser	Gly	Lys	Ala	Cys
1				5					10					15	

Lys	Asn	Leu	Lys	Cys	Cys	Ser
			20			

<210> 492

<211> 23

<212> PRT

<213> Conus bullatus

<400> 492

Val	Thr	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Glu	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

<210> 493

<211> 23

<212> PRT

<213> Conus bullatus

<400> 493

Val	Gly	Asp	Arg	Cys	Cys	Lys	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp	Cys
1				5					10					15	

Arg	Asp	His	Ser	Arg	Cys	Cys
			20			

<210> 494

<211> 24

<212> PRT

<213> Conus bullatus

<400> 494

Val	Gly	Glu	Arg	Cys	Cys	Lys	Asn	Gly	Lys	Arg	Gly	Cys	Gly	Arg	Trp
1				5					10					15	

Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
			20				

<210> 495

<211> 26

<212> PRT

<213> Conus bullatus

<400> 495

Ile	Val	Asp	Arg	Cys	Cys	Asn	Lys	Gly	Asn	Gly	Lys	Arg	Gly	Cys	Ser
1				5					10					15	

Arg	Trp	Cys	Arg	Asp	His	Ser	Arg	Cys	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

25

```

<400> 496
Val Gly Cys Cys Arg Pro Lys Pro Asn Gly Gln Met Met Cys Asp Arg
1      5      10      15
Trp Cys Glu Lys Asn Ser Arg Cys Cys
      20      25

```

```

<400> 497
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Lys Asp Arg Gln Cys Lys
1      5      10      15
Pro Gln Arg Cys Cys Ala
      20

```

```

<400> 498
Gly Arg Asp Cys Cys Thr Pro Pro Arg Lys Cys Arg Asp Arg Ala Cys
1          5          10          15
Lys Pro Gln Arg Cys Cys Gly
          20

```

```
<400> 499
Glx Arg Leu Cys Cys Gly Phe Pro Lys Ser Cys Arg Ser Arg Gln Cys
1          5          10          15
Lys Pro His Arg Cys Cys
          20
```

```
<400> 500
Arg Asp Cys Cys Thr Pro Pro Lys Lys Cys Arg Asp Arg Gln Cys Lys
1          5          10          15
Pro Ala Arg Cys Cys Gly
          20
```

<210>	501
<211>	22
<212>	PRT

<400> 501

Met Arg Lys Ala Cys Cys
20

<210> 502

<211> 22

<212> PRT

<213> Conus laterculatus

<400> 502

Lys Arg Lys Ala Cys Cys
20

<210> 503

<211> 22

<212> PRT

<213> Conus geographus

 $\langle 220 \rangle$

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$

<223> Xaa is Hyp

<400> 503

Xaa Gln Arg Cys Cys Ala
20

<210> 504

<211> 22

<212> PRT

<213> *Conus geographus*

 $\langle 220 \rangle$

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$

<223> Xaa is Hyp

<400> 504

Xaa Met Lys Cys Cys Ala
20

<210> 505

<211> 22

<212> PRT

<213> Conus geographus

 $\langle 220 \rangle$

<221> PEPTIDE

 $\langle 222 \rangle \quad (1) \dots (22)$

<223> Xaa is Hyp

Xaa Leu Lys Cys Cys Ala
20

<213> Conus purpurascens

<223> Xaa is Hyp

Lys Xaa His Arg Cys Cys
20

<213> Conus magus

Pro Gln Arg Cys Cys Ala
20

<213> Conus marmoreus

Lys Pro Ala Arg Cys Cys Gly Pro
20

<213> Conus nobilis

Lys Asn Leu Lys Cys Cys Ser
20

<213> Conus parius

Lys Pro Ala Arg Cys Cys Gly Pro
20

<213> Conus parius

Pro Ala Arg Cys Cys Gly Pro
20

<213> Conus radiatus

<223> Xaa is Hyp

Cys Lys Arg Asn Xaa Cys Cys Thr
20

<213> Conus radiatus

<223> Xaa is Hyp

Arg Ser Lys Xaa Cys Cys Lys Ser
20

<213> Conus radiatus

Lys Pro Ala Arg Cys Cys Gly Pro
20

<210> 515
 <211> 23
 <212> PRT
 <213> Conus stercusmuscarum

<400> 515
 Glx Lys Cys Cys Thr Gly Lys Lys Gly Ser Cys Ser Gly Lys Ala Cys
 1 5 10 15

Lys Asn Leu Lys Cys Cys Ser
 20

<210> 516
 <211> 21
 <212> PRT
 <213> Conus tulipa

<220>
 <221> PEPTIDE
 <222> (1)..(21)
 <223> Xaa is Hyp

<400> 516
 His Gly Cys Cys Lys Gly Xaa Glu Gly Cys Ser Ser Arg Glu Cys Arg
 1 5 10 15

Xaa Gln His Cys Cys
 20

<210> 517
 <211> 21
 <212> PRT
 <213> Conus tulipa

<400> 517
 His Gly Cys Cys Glu Gly Pro Lys Gly Cys Ser Ser Arg Glu Cys Arg
 1 5 10 15

Pro Gln His Cys Cys
 20

<210> 518
 <211> 23
 <212> PRT
 <213> Conus wittigi

<400> 518
 Leu Pro Ser Cys Cys Asp Phe Glu Arg Leu Cys Val Val Pro Ala Cys
 1 5 10 15

Ile Arg His Gln Cys Cys Thr
 20

<210> 519
 <211> 17
 <212> PRT
 <213> Conus omaria

<400> 519
 Cys Cys Lys Tyr Gly Trp Thr Cys Leu Leu Gly Cys Thr Pro Cys Asp
 1 5 10 15

Cys

<210> 520

```
<211> 17
<212> PRT
<213> Conus omaria
```

<400> 520

Cys Cys Arg Tyr Gly Trp Thr Cys Trp Leu Gly Cys Thr Pro Cys Gly
1 5 10 15

Cys

[illegible]